



1

SEQUENCE LISTING

<10> METZ, JAMES G.
LARDIZABAL, KATHRYN D.
LASSNER, MICHAEL

<120> NUCLEIC ACID SEQUENCES ENCODING A PLANT CYTOPLASMIC
PROTEIN INVOLVED IN FATTY ACYL-COA METABOLISM

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<140> 08/657,749
<141> 1996-05-30

<150> PCT/US94/13686
<151> 1994-11-30

<150> 08/265,047
<151> 1994-06-23

<150> 08/160,602
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<150> PCT/US92/09863
<151> 1992-11-13

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<170> PatentIn Ver. 2.1

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Tyr Leu Leu Leu Arg Ala Thr Asp Asp Glu Thr Ala Ala Leu Arg Leu
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Gln Asn Glu Val Phe Gly Lys Glu Leu Phe Lys Val Leu Lys Gln Asn
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Leu Gly Ala Asn Phe Tyr Ser Phe Val Ser Glu Lys Val Thr Val Val
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Pro Gly Asp Ile Thr Gly Glu Asp Leu Cys Leu Lys Asp Val Asn Leu
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Thr Ile Asn Phe Ile Glu Arg Tyr Asp Val Ser Leu Leu Ile Asn Thr
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aga tta ggt ctg gac att aat gta gag aag aaa ctt gtg gag gca aaa	688
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Ile Asn Glu Leu Gln Ala Ala Gly Ala Thr Glu Lys Ser Ile Lys Ser	
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Asn Val Tyr Val Phe Thr Lys Ala Leu Gly Glu Met Leu Leu Met Gln	
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Tyr Lys Gly Asp Ile Pro Leu Thr Ile Ile Arg Pro Thr Ile Ile Thr	
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agc act ttt aaa gag ccc ttt cct ggt tgg gtt gaa ggt gtc agg acc	928
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Pro Trp Ile Asn Pro Asp Arg Asn Pro Val His Val Gly Arg Ala Met	
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 Ile Val Glu Ala Asp Met Phe Tyr Phe Asp Pro Arg Ala Ile Asn Trp
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 480 485 490
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 Leu Asn
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Tyr	Ser	Phe	Val	Ser	Glu	Lys	Val	Thr	Val	Val	Pro	Gly	Asp	Ile	Thr	85	90	95	
Gly	Glu	Asp	Leu	Cys	Leu	Lys	Asp	Val	Asn	Leu	Lys	Glu	Glu	Met	Trp	100	105	110	
Arg	Glu	Ile	Asp	Val	Val	Val	Asn	Leu	Ala	Ala	Thr	Ile	Asn	Phe	Ile	115	120	125	
Glu	Arg	Tyr	Asp	Val	Ser	Leu	Leu	Ile	Asn	Thr	Tyr	Gly	Ala	Lys	Tyr	130	135	140	
Val	Leu	Asp	Phe	Ala	Lys	Lys	Cys	Asn	Lys	Leu	Lys	Ile	Phe	Val	His	145	150	155	160
Val	Ser	Thr	Ala	Tyr	Val	Ser	Gly	Glu	Lys	Asn	Gly	Leu	Ile	Leu	Glu	165	170	175	
Lys	Pro	Tyr	Tyr	Met	Gly	Glu	Ser	Leu	Asn	Gly	Arg	Leu	Gly	Leu	Asp	180	185	190	
Ile	Asn	Val	Glu	Lys	Lys	Leu	Val	Glu	Ala	Lys	Ile	Asn	Glu	Leu	Gln	195	200	205	
Ala	Ala	Gly	Ala	Thr	Glu	Lys	Ser	Ile	Lys	Ser	Thr	Met	Lys	Asp	Met	210	215	220	
Gly	Ile	Glu	Arg	Ala	Arg	His	Trp	Gly	Trp	Pro	Asn	Val	Tyr	Val	Phe	225	230	235	240
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Pro	Phe	Pro	Gly	Trp	Val	Glu	Gly	Val	Arg	Thr	Ile	Asp	Asn	Val	Pro	275	280	285	
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 Asp Arg Asn Pro Val His Val Gly Arg Ala Met Val Phe Ser Ser Phe
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 Val Leu Glu Ile Ala Asn Thr Ile Phe Cys Gln Trp Phe Lys Gly Lys
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 Tyr Met Asp Leu Lys Arg Lys Thr Arg Leu Leu Leu Arg Leu Val Asp
 420 425 430
 Ile Tyr Lys Pro Tyr Leu Phe Phe Gln Gly Ile Phe Asp Asp Met Asn
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 Thr Glu Lys Leu Arg Ile Ala Ala Lys Glu Ser Ile Val Glu Ala Asp
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His Val Lys Leu Gly Tyr His Tyr Leu Ile Ser Asn Ala Leu Phe Leu	
40 45 50	
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Val Phe Ile Pro Leu Leu Gly Leu Ala Ser Ala His Leu Ser Ser Phe	
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Ser Ala His Asp Leu Ser Leu Leu Phe Asp Leu Leu Arg Arg Asn Leu	
75 80 85	
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Leu Pro Val Val Val Cys Ser Phe Leu Phe Val Leu Leu Ala Thr Leu	
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His Phe Leu Thr Arg Pro Arg Asn Val Tyr Leu Val Asp Phe Gly Cys	
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Arg Lys Ile Leu Glu Arg Ala Gly Met Gly Arg Glu Thr Tyr Val Pro	
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Glu Ser Val Thr Lys Val Pro Ala Glu Pro Ser Ile Ala Ala Ala Arg	
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Cys Ser Ala Gly Leu Ile Ser Ile Asp Leu Ala Lys Asp Leu Leu Gln	
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gtt tac cgt aaa aac aca tat gtg tta gta gtg agc acg gaa aac atg	872
Val Tyr Arg Lys Asn Thr Tyr Val Leu Val Val Ser Thr Glu Asn Met	
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Thr Leu Asn Trp Tyr Trp Gly Asn Asp Arg Ser Met Leu Ile Thr Asn	
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Cys Leu Phe Arg Met Gly Gly Ala Ala Ile Ile Leu Ser Asn Arg Trp	
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425 430 435	


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Gly Asp Arg Thr Trp Met Ile Gly Phe Gly Ser Gly Phe Lys Cys Asn
475 480 485

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Ser Val Val Trp Arg Ala Leu Arg Ser Val Asn Pro Ala Arg Glu Lys
490 495 500

aat cct tgg atg gat gaa att gag aag ttc cct gtc cat gtg cct aaa 1592
Asn Pro Trp Met Asp Glu Ile Glu Lys Phe Pro Val His Val Pro Lys
505 510 515

atc gca cct atc gct tcg tagaactgct aggatgtgat tagtaatgaa 1640
Ile Ala Pro Ile Ala Ser
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Ala His Leu Ser Ser Phe Ser Ala His Asp Leu Ser Leu Leu Phe Asp
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 His Glu Met Phe Met Asp Arg Thr Ser Arg Ala Gly Ser Phe Ser Lys
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 Glu Asn Ile Glu Phe Gln Arg Lys Ile Leu Glu Arg Ala Gly Met Gly
 145 150 155 160
 Arg Glu Thr Tyr Val Pro Glu Ser Val Thr Lys Val Pro Ala Glu Pro
 165 170 175
 Ser Ile Ala Ala Ala Arg Ala Glu Ala Glu Glu Val Met Tyr Gly Ala
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 Ser Met Ile Val Asn His Tyr Lys Xaa Arg Gly Asn Ile Leu Ser Tyr
 225 230 235 240
 Asn Leu Gly Gly Met Gly Cys Ser Ala Gly Leu Ile Ser Ile Asp Leu
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 Ala Lys Asp Leu Leu Gln Val Tyr Arg Lys Asn Thr Tyr Val Leu Val
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 Val Ser Thr Glu Asn Met Thr Leu Asn Trp Tyr Trp Gly Asn Asp Arg
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 355 360 365

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 Thr Pro Trp His Leu Glu Pro Ser Arg Met Thr Leu Tyr Arg Phe Gly
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 Lys Gly Arg Ile Arg Lys Gly Asp Arg Thr Trp Met Ile Gly Phe Gly
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 Ser Gly Phe Lys Cys Asn Ser Val Val Trp Arg Ala Leu Arg Ser Val
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 Thr Thr Met Thr Thr Thr Thr Thr Thr Thr Ala Thr Leu Pro Asn Phe Lys
 15 20 25 30
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 Ser Ser Ile Asn Leu His His Val Lys Leu Gly Tyr His Tyr Leu Ile
 35 40 45

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Ala His Leu Ser Ser Phe Ser Ala His Asp Leu Ser Leu Leu Phe Asp	
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Leu Leu Arg Arg Asn Leu Leu Pro Val Val Val Cys Ser Phe Leu Phe	
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95 100 105 110	
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130 135 140	
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Ser Ile Ala Ala Ala Arg Ala Glu Ala Glu Glu Val Met Tyr Gly Ala	
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Ile Asp Glu Val Leu Glu Lys Thr Gly Val Lys Pro Lys Gln Ile Gly	
195 200 205	
ata ctg gtg gtg aac tgc agc ttg ttt aac cca acg ccg tcg ctg tca	675
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Ser Met Ile Val Asn His Tyr Lys Leu Arg Gly Asn Ile Leu Ser Tyr	
225 230 235	
aat ctt ggt ggc atg ggt tgc agt gct ggg ctc att tcc att gat ctt	771
Asn Leu Gly Gly Met Gly Cys Ser Ala Gly Leu Ile Ser Ile Asp Leu	
240 245 250	

gcc aag gac ctc cta cag gtt tac cgt aac aca tat gtg tta gta gtg Ala Lys Asp Leu Leu Gln Val Tyr Arg Asn Thr Tyr Val Leu Val Val 255 260 265 270	819
agc aca gaa aac atg acc ctt aat tgg tac tgg ggc aat gac cgc tcc Ser Thr Glu Asn Met Thr Leu Asn Trp Tyr Trp Gly Asn Asp Arg Ser 275 280 285	867
atg ctt atc acc aac tgc cta ttt cgc atg ggt ggc gct gcc atc atc Met Leu Ile Thr Asn Cys Leu Phe Arg Met Gly Gly Ala Ala Ile Ile 290 295 300	915
ctc tca aac cgc tgg cgt gat cgt cgc cga tcc aag tac caa ctc ctt Leu Ser Asn Arg Trp Arg Asp Arg Arg Arg Ser Lys Tyr Gln Leu Leu 305 310 315	963
cac aca gta cgc acc cac aag ggc gct gac gac aag tcc tat aga tgc His Thr Val Arg Thr His Lys Gly Ala Asp Asp Lys Ser Tyr Arg Cys 320 325 330	1011
gtc tta caa caa gaa gat gaa aat aac aag gta ggt gtt gcc tta tcc Val Leu Gln Gln Glu Asp Glu Asn Asn Lys Val Gly Val Ala Leu Ser 335 340 345 350	1059
aag gat ctg atg gca gtt gcc ggt gaa gcc cta aag gcc aac atc acg Lys Asp Leu Met Ala Val Ala Gly Glu Ala Leu Lys Ala Asn Ile Thr 355 360 365	1107
acc ctt ggt ccc ctc gtg ctc ccc atg tca gaa caa ctc ctc ttc ttt Thr Leu Gly Pro Leu Val Leu Pro Met Ser Glu Gln Leu Leu Phe Phe 370 375 380	1155
gcc acc tta gtg gca cgt aag gtc ttc aag atg acg aac gtg aag cca Ala Thr Leu Val Ala Arg Lys Val Phe Lys Met Thr Asn Val Lys Pro 385 390 395	1203
tac atc cca gat ttc aag ttg gca gcg aag cac ttc tgc atc cat gca Tyr Ile Pro Asp Phe Lys Leu Ala Ala Lys His Phe Cys Ile His Ala 400 405 410	1251
gga ggc aaa gca gtg ttg gat gag ctc gag acg aac ttg gag ttg acg Gly Gly Lys Ala Val Leu Asp Glu Leu Glu Thr Asn Leu Glu Leu Thr 415 420 425 430	1299
cca tgg cac ctt gaa ccc tcg agg atg aca ctg tat agg ttt ggg aac Pro Trp His Leu Glu Pro Ser Arg Met Thr Leu Tyr Arg Phe Gly Asn 435 440 445	1347
aca tcg agt agc tca tta tgg tac gag ttg gca tac gct gaa gca aaa Thr Ser Ser Ser Ser Leu Trp Tyr Glu Leu Ala Tyr Ala Glu Ala Lys 450 455 460	1395

ggg agg atc cgt aag ggt gat cga act tgg atg att gga ttt ggt tca 1443
Gly Arg Ile Arg Lys Gly Asp Arg Thr Trp Met Ile Gly Phe Gly Ser
465 470 475

ggt ttc aag tgt aac agt gtt gtg tgg agg gct ttg agg agt gtc aat 1491
 Gly Phe Lys Cys Asn Ser Val Val Trp Arg Ala Leu Arg Ser Val Asn
 480 485 490

ccg gct aga gag aag aat cct tgg atg gat gaa att gag aat ttc cct 1539
Pro Ala Arg Glu Lys Asn Pro Trp Met Asp Glu Ile Glu Asn Phe Pro
495 500 505 510

gtc cat gtg cct aaa atc gca cct atc gct tcg tagaactgct aggatgtgat 1592
Val His Val Pro Lys Ile Ala Pro Ile Ala Ser
515 520

tagtaatgaa aaatgtgtat tatgttagtg atgtagaaaa agaaacttta gttgatgggt 1652

gagaacatgt ctcattgaga ataacgtgtg catcgttgtg ttgaatttga atttgagtat 1712

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tacgctttct t 1783

<210> 6

<211> 521

<212> PRT

<213> *Simmondsia chinensis*

<400> 6

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20 25 30

Ile Asn Leu His His Val Lys Leu Gly Tyr His Tyr Leu Ile Ser Asn
35 40 45

Ala Leu Phe Leu Val Phe Ile Pro Leu Leu Gly Leu Ala Ser Ala His
50 55 60

Leu Ser Ser Phe Ser Ala His Asp Leu Ser Leu Leu Phe Asp Leu Leu
65 70 75 80

Arg Arg Asn Leu Leu Pro Val Val Val Cys Ser Phe Leu Phe Val Leu
85 90 95

Leu Ala Thr Leu His Phe Leu Thr Arg Pro Arg Asn Val Tyr Leu Val
100 105 110

Asp Phe Ala Cys Tyr Lys Pro His Pro Asn Leu Ile Thr Ser His Glu
115 120 125

Met	Phe	Met	Asp	Arg	Thr	Ser	Arg	Ala	Gly	Ser	Phe	Ser	Lys	Glu	Asn	130	135	140
Ile	Glu	Phe	Gln	Arg	Lys	Ile	Leu	Glu	Arg	Ala	Gly	Met	Gly	Arg	Glu	145	150	155
Thr	Tyr	Val	Pro	Glu	Ser	Val	Thr	Lys	Val	Pro	Pro	Glu	Pro	Ser	Ile	165	170	175
Ala	Ala	Ala	Arg	Ala	Glu	Ala	Glu	Glu	Val	Met	Tyr	Gly	Ala	Ile	Asp	180	185	190
Glu	Val	Leu	Glu	Lys	Thr	Gly	Val	Lys	Pro	Lys	Gln	Ile	Gly	Ile	Leu	195	200	205
Val	Val	Asn	Cys	Ser	Leu	Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ser	Met	210	215	220
Ile	Val	Asn	His	Tyr	Lys	Leu	Arg	Gly	Asn	Ile	Leu	Ser	Tyr	Asn	Leu	225	230	235
Gly	Gly	Met	Gly	Cys	Ser	Ala	Gly	Leu	Ile	Ser	Ile	Asp	Leu	Ala	Lys	245	250	255
Asp	Leu	Leu	Gln	Val	Tyr	Arg	Asn	Thr	Tyr	Val	Leu	Val	Val	Ser	Thr	260	265	270
Glu	Asn	Met	Thr	Leu	Asn	Trp	Tyr	Trp	Gly	Asn	Asp	Arg	Ser	Met	Leu	275	280	285
Ile	Thr	Asn	Cys	Leu	Phe	Arg	Met	Gly	Gly	Ala	Ala	Ile	Ile	Leu	Ser	290	295	300
Asn	Arg	Trp	Arg	Asp	Arg	Arg	Arg	Ser	Lys	Tyr	Gln	Leu	Leu	His	Thr	305	310	315
Val	Arg	Thr	His	Lys	Gly	Ala	Asp	Asp	Lys	Ser	Tyr	Arg	Cys	Val	Leu	325	330	335
Gln	Gln	Glu	Asp	Glu	Asn	Asn	Lys	Val	Gly	Val	Ala	Leu	Ser	Lys	Asp	340	345	350
Leu	Met	Ala	Val	Ala	Gly	Glu	Ala	Leu	Lys	Ala	Asn	Ile	Thr	Thr	Leu	355	360	365
Gly	Pro	Leu	Val	Leu	Pro	Met	Ser	Glu	Gln	Leu	Leu	Phe	Phe	Ala	Thr	370	375	380
Leu	Val	Ala	Arg	Lys	Val	Phe	Lys	Met	Thr	Asn	Val	Lys	Pro	Tyr	Ile	385	390	395
Pro	Asp	Phe	Lys	Leu	Ala	Ala	Lys	His	Phe	Cys	Ile	His	Ala	Gly	Gly	405	410	415

Lys Ala Val Leu Asp Glu Leu Glu Thr Asn Leu Glu Leu Thr Pro Trp
 420 425 430
 His Leu Glu Pro Ser Arg Met Thr Leu Tyr Arg Phe Gly Asn Thr Ser
 435 440 445
 Ser Ser Ser Leu Trp Tyr Glu Leu Ala Tyr Ala Glu Ala Lys Gly Arg
 450 455 460
 Ile Arg Lys Gly Asp Arg Thr Trp Met Ile Gly Phe Gly Ser Gly Phe
 465 470 475 480
 Lys Cys Asn Ser Val Val Trp Arg Ala Leu Arg Ser Val Asn Pro Ala
 485 490 495
 Arg Glu Lys Asn Pro Trp Met Asp Glu Ile Glu Asn Phe Pro Val His
 500 505 510
 Val Pro Lys Ile Ala Pro Ile Ala Ser
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<210> 7

<211> 1647

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oleosin
expression cassette

<400> 7

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gttatgtccc gtcgtctccg aacagacatc ctcgtagctc ggattatcga cgaatccatg 180
gctataccca acctccgtct tcgtcacgcc tggaaacctc tggtagcga attccgctcc 240
ccagaagcaa ccggcgccga attgcgcgaa ttgctgacct ggagacggaa catcgctcgtc 300
gggtccttgc gcgattgcgg cggaagccgg gtcggttgg ggacgagacc cgaatccgag 360
cctggtgaag aggttgttca tcggagattt atagacggag atggatcgag cggttttggg 420
gaaaggggaa gtgggttgg ctcttttgg tagagagagt gcagctttgg agagagactg 480
gagaggttta gagagagacg cggcggatat taccggagga gaggcgacga gagatagcat 540
tatcgaaggg gagggagaaa gagtgcgtg gagaaataag aaaccgttaa gagtcggata 600
tttatcatat taaaagccca atgggcctga acccatttaa acaagacaga taaatgggcc 660
gtgtgttaag ttaacagagt gttaacgttc ggtttcaaat gccaacgcca taggaacaaa 720
acaaacgtgt cctcaagtaa acccctgccg ttacacctc aatggctgca tggatgaagcc 780
attaacacgt ggcgtaggat gcatgacgac gccattgaca cctgactctc ttcccttctc 840
ttcatatata tctaatacat tcaactactc attgtcatag ctattcggaa aatacatata 900
catccttttc tcttcgatct ctctcaattc acaagaagca aagtcgacgg atccctgcag 960
taaattacgc catgactatt ttcatagtcc aataaggctg atgtcgggag tccagtttat 1020
gagcaataag gtgttttagaa tttgatcaat gtttataata aaagggggaa gatgatataca 1080
cagtcttttg ttcttttttg cttttgttaa atttgtgtgt ttctatttgt aaacctcctg 1140
tatatgttgt acttctttcc ctttttaagt ggtatcgtct atatggtaaa acgttatgtt 1200

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tggctctttcc ttttctctgt ttaggataaa aagactgcat gttttatctt tagttatatt 1260
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agctgaactg aacagctggc aatgtgaaca ctggatgcaa gatcagatgt gaagatctct 1380
aatatgggtg tgggattgaa catatcgtgt ctatatTTTT gttggcatta agctcttaac 1440
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aaccctaaact tcaaaaacag taggccacct gaattgcctt atcgaataag agtttgtttc 1560
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<211> 1810

<212> DNA

<213> Brassica sp.

<220>

<221> CDS

<222> (4)..(1647)

<400> 8

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aac cgt ggg atc gaa cct tcc ggt cca aac gcc ggt tca cca acg ttc 96
Asn Arg Gly Ile Glu Pro Ser Gly Pro Asn Ala Gly Ser Pro Thr Phe
20 25 30

tcg gtc aga gtc cgg aga cgt tta ccg gat ttt ctt caa tcc gta aac 144
Ser Val Arg Val Arg Arg Arg Leu Pro Asp Phe Leu Gln Ser Val Asn
35 40 45

ttg aag tac gtg aaa ctt ggt tat cac tac ctc ata aac cat gcg gtt 192
Leu Lys Tyr Val Lys Leu Gly Tyr His Tyr Leu Ile Asn His Ala Val
50 55 60

tac ttg gcg acg ata ccg gtt ctt gtg ctt gtg ttt agt gcc gaa gtt 240
Tyr Leu Ala Thr Ile Pro Val Leu Val Leu Val Phe Ser Ala Glu Val
65 70 75

ggg agt tta agc gga gaa gag att tgg aag aag ctt tgg gac tat gat 288
Gly Ser Leu Ser Gly Glu Glu Ile Trp Lys Lys Leu Trp Asp Tyr Asp
80 85 90 95

atc gca acc gtc atc gga ttc ttc ggt gtc ttt gtc ttg acc gtt tgc 336
Ile Ala Thr Val Ile Gly Phe Phe Gly Val Phe Val Leu Thr Val Cys
100 105 110

gtc tac ttc atg tct cgt cca cga tct gtt tat ctc att gac ttc gct 384
Val Tyr Phe Met Ser Arg Pro Arg Ser Val Tyr Leu Ile Asp Phe Ala
115 120 125

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tgt ttc aag cct tcc gat gaa ctt aag gtg aca aga gaa gag ttc ata	432
Cys Phe Lys Pro Ser Asp Glu Leu Lys Val Thr Arg Glu Glu Phe Ile	
130 135 140	
gat cta gct aga aaa tca ggc aag ttc gac gaa gag atc ctc gga ttc	480
Asp Leu Ala Arg Lys Ser Gly Lys Phe Asp Glu Glu Ile Leu Gly Phe	
145 150 155	
aag aag agg atc ctt caa gcc tca gga ata ggc gat gaa acg tac gtc	528
Lys Lys Arg Ile Leu Gln Ala Ser Gly Ile Glu Asp Glu Thr Tyr Val	
160 165 170 175	
cca aga tca atc tct tcg tcg gaa aac aca aca acg atg aaa gaa ggt	576
Pro Arg Ser Ile Ser Ser Ser Glu Asn Thr Thr Thr Met Lys Glu Gly	
180 185 190	
cgt gaa gaa gcc tcg atg atg ata ttc ggc gca ctc gac gaa ctc ttc	624
Arg Glu Glu Ala Ser Met Met Ile Phe Gly Ala Leu Asp Glu Leu Phe	
195 200 205	
gag aag aca cgt gtc aaa ccg aaa gac gta ggt gtc ctc gtg gtt aac	672
Glu Lys Thr Arg Val Lys Pro Lys Asp Val Gly Val Leu Val Val Asn	
210 215 220	
tgc agt atc ttt aac ccg act ccg tca ctc tcc gcg atg gtg att aac	720
Cys Ser Ile Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Ile Asn	
225 230 235	
cac tac aag atg aga ggg aac ata ctt agc tac aac cta gga ggg atg	768
His Tyr Lys Met Arg Gly Asn Ile Leu Ser Tyr Asn Leu Gly Gly Met	
240 245 250 255	
ggg tgc tca gca gga atc ata gcc gtt gat ctt gct cgt gac atg ctt	816
Gly Cys Ser Ala Gly Ile Ile Ala Val Asp Leu Ala Arg Asp Met Leu	
260 265 270	
cag tct aac ccg aat agt tac gcg gtg gtt gtg agt acc gag atg gtt	864
Gln Ser Asn Pro Asn Ser Tyr Ala Val Val Val Ser Thr Glu Met Val	
275 280 285	
ggg tat aat tgg tac gtg gga cgt gac aag tca atg gtt ata cct aac	912
Gly Tyr Asn Trp Tyr Val Gly Arg Asp Lys Ser Met Val Ile Pro Asn	
290 295 300	
tgc ttc ttt agg atg ggt tgc tcc gcc gtt atg ctg tct aac cgc cgc	960
Cys Phe Phe Arg Met Gly Cys Ser Ala Val Met Leu Ser Asn Arg Arg	
305 310 315	
cgt gac ttc cgc cat gct aag tac cgc ctt gag cac att gtc cgg act	1008
Arg Asp Phe Arg His Ala Lys Tyr Arg Leu Glu His Ile Val Arg Thr	
320 325 330 335	

cac aag gct gcc gac gac cgt agc ttc agg agt gtg tac cag gaa gaa	1056
His Lys Ala Ala Asp Asp Arg Ser Phe Arg Ser Val Tyr Gln Glu Glu	
340 345 350	
gat gaa caa gga ttc aag gga tta aaa ata agc aga gac cta atg gaa	1104
Asp Glu Gln Gly Phe Lys Gly Leu Lys Ile Ser Arg Asp Leu Met Glu	
355 360 365	
gtt gga ggt gaa gct ctc aag acc aac atc acc acc tta ggc cct ctc	1152
Val Gly Gly Glu Ala Leu Lys Thr Asn Ile Thr Thr Leu Gly Pro Leu	
370 375 380	
gtc ctt cct ttc tcc gag cag ctt ctc ttc ttt gcc gct ttg atc cgt	1200
Val Leu Pro Phe Ser Glu Gln Leu Leu Phe Phe Ala Ala Leu Ile Arg	
385 390 395	
aga act ttc tca ccc gcc gcc aaa act acc acc acc tcc tcc tca gcc	1248
Arg Thr Phe Ser Pro Ala Ala Lys Thr Thr Thr Thr Ser Ser Ser Ala	
400 405 410 415	
act gcg aaa atc aac gga gcc aag tcg tca tcc tcc tct gat cta tcc	1296
Thr Ala Lys Ile Asn Gly Ala Lys Ser Ser Ser Ser Ser Asp Leu Ser	
420 425 430	
aag ccg tac atc ccg gac tac aag ctt gcc ttc gag cat ttc tgc ttc	1344
Lys Pro Tyr Ile Pro Asp Tyr Lys Leu Ala Phe Glu His Phe Cys Phe	
435 440 445	
cac gcg gca agc aaa gcg gtg ctt gag gag ctt cag aag aat cta ggc	1392
His Ala Ala Ser Lys Ala Val Leu Glu Glu Leu Gln Lys Asn Leu Gly	
450 455 460	
ttg agt gat gag aac atg gag gct tct aag atg act tta cac agg ttt	1440
Leu Ser Asp Glu Asn Met Glu Ala Ser Lys Met Thr Leu His Arg Phe	
465 470 475	
gga aac act tcc agc agt gga atc tgg tac gag ctt gct tac atg gag	1488
Gly Asn Thr Ser Ser Ser Gly Ile Trp Tyr Glu Leu Ala Tyr Met Glu	
480 485 490 495	
gcc aag gag agt gtt cgt aga ggc gat agg gtt tgg cag att gct ttt	1536
Ala Lys Glu Ser Val Arg Arg Gly Asp Arg Val Trp Gln Ile Ala Phe	
500 505 510	
ggg tca ggt ttt aag tgt aac agt gtg gtt tgg aag gca atg agg aag	1584
Gly Ser Gly Phe Lys Cys Asn Ser Val Val Trp Lys Ala Met Arg Lys	
515 520 525	
gtg aag aag ccg gca agg aac aat cct tgg gtt gat tgc att aac cgt	1632
Val Lys Lys Pro Ala Arg Asn Asn Pro Trp Val Asp Cys Ile Asn Arg	
530 535 540	

tac cct gtc gct ctc tgatcattta tttttaaaat tattatttct tcttaattaa 1687
 Tyr Pro Val Ala Leu
 545

atcatctatg atctctcttc cttgttggtg gatgatagac gtttgtttgc tggtcattcg 1747
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 aaa 1810

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 <212> PRT
 <213> Brassica sp.

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 Val Arg Val Arg Arg Arg Leu Pro Asp Phe Leu Gln Ser Val Asn Leu
 35 40 45
 Lys Tyr Val Lys Leu Gly Tyr His Tyr Leu Ile Asn His Ala Val Tyr
 50 55 60
 Leu Ala Thr Ile Pro Val Leu Val Leu Val Phe Ser Ala Glu Val Gly
 65 70 75 80
 Ser Leu Ser Gly Glu Glu Ile Trp Lys Lys Leu Trp Asp Tyr Asp Ile
 85 90 95
 Ala Thr Val Ile Gly Phe Phe Gly Val Phe Val Leu Thr Val Cys Val
 100 105 110
 Tyr Phe Met Ser Arg Pro Arg Ser Val Tyr Leu Ile Asp Phe Ala Cys
 115 120 125
 Phe Lys Pro Ser Asp Glu Leu Lys Val Thr Arg Glu Glu Phe Ile Asp
 130 135 140
 Leu Ala Arg Lys Ser Gly Lys Phe Asp Glu Glu Ile Leu Gly Phe Lys
 145 150 155 160
 Lys Arg Ile Leu Gln Ala Ser Gly Ile Gly Asp Glu Thr Tyr Val Pro
 165 170 175
 Arg Ser Ile Ser Ser Ser Glu Asn Thr Thr Thr Met Lys Glu Gly Arg
 180 185 190

Glu Glu Ala Ser Met Met Ile Phe Gly Ala Leu Asp Glu Leu Phe Glu
 195 200 205
 Lys Thr Arg Val Lys Pro Lys Asp Val Gly Val Leu Val Val Asn Cys
 210 215 220
 Ser Ile Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Ile Asn His
 225 230 235 240
 Tyr Lys Met Arg Gly Asn Ile Leu Ser Tyr Asn Leu Gly Gly Met Gly
 245 250 255
 Cys Ser Ala Gly Ile Ile Ala Val Asp Leu Ala Arg Asp Met Leu Gln
 260 265 270
 Ser Asn Pro Asn Ser Tyr Ala Val Val Val Ser Thr Glu Met Val Gly
 275 280 285
 Tyr Asn Trp Tyr Val Gly Arg Asp Lys Ser Met Val Ile Pro Asn Cys
 290 295 300
 Phe Phe Arg Met Gly Cys Ser Ala Val Met Leu Ser Asn Arg Arg Arg
 305 310 315 320
 Asp Phe Arg His Ala Lys Tyr Arg Leu Glu His Ile Val Arg Thr His
 325 330 335
 Lys Ala Ala Asp Asp Arg Ser Phe Arg Ser Val Tyr Gln Glu Glu Asp
 340 345 350
 Glu Gln Gly Phe Lys Gly Leu Lys Ile Ser Arg Asp Leu Met Glu Val
 355 360 365
 Gly Gly Glu Ala Leu Lys Thr Asn Ile Thr Thr Leu Gly Pro Leu Val
 370 375 380
 Leu Pro Phe Ser Glu Gln Leu Leu Phe Phe Ala Ala Leu Ile Arg Arg
 385 390 395 400
 Thr Phe Ser Pro Ala Ala Lys Thr Thr Thr Thr Ser Ser Ser Ala Thr
 405 410 415
 Ala Lys Ile Asn Gly Ala Lys Ser Ser Ser Ser Ser Asp Leu Ser Lys
 420 425 430
 Pro Tyr Ile Pro Asp Tyr Lys Leu Ala Phe Glu His Phe Cys Phe His
 435 440 445
 Ala Ala Ser Lys Ala Val Leu Glu Glu Leu Gln Lys Asn Leu Gly Leu
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 Ser Asp Glu Asn Met Glu Ala Ser Lys Met Thr Leu His Arg Phe Gly
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<213> Brassica sp.
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Thr	Asn	Leu	Phe	Asn	Leu	Cys	Phe	Phe	Pro	Leu	Thr	Ala	Ile	Val	Ala	
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Gly	Lys	Ala	Tyr	Arg	Leu	Thr	Ile	Asp	Asp	Leu	His	His	Leu	Tyr	Tyr	
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Ser	Tyr	Leu	Gln	His	Asn	Leu	Ile	Thr	Ile	Ala	Pro	Leu	Phe	Ala	Phe	
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Ser	Ile	Ser	Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Val	Arg	Lys	Ala	Asp	
	95				100					105				110		

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115 120 125	
agg aag att caa gaa cgt tca ggt cta ggc gat gaa acc cac ggg ccc	435
Arg Lys Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro	
130 135 140	
gag ggg ctg ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt	483
Glu Gly Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg	
145 150 155	
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Glu Glu Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys	
160 165 170	
aac acc aat gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca	579
Asn Thr Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser	
175 180 185 190	
agc atg ttt aat cca act cct tcg ctc tcc gcg atg gtc gtt aac act	627
Ser Met Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr	
195 200 205	
ttc aag ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt	675
Phe Lys Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly	
210 215 220	
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Cys Ser Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His	
225 230 235	
gtc cat aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act	771
Val His Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr	
240 245 250	
tat aac att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc	819
Tyr Asn Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys	
255 260 265 270	
ttg ttc cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct aga	867
Leu Phe Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Arg	
275 280 285	
gat cgt aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat	915
Asp Arg Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His	
290 295 300	
acc gga gct gac gac aag tct ttt cgt tgc gtg caa caa gga gac gtt	963
Thr Gly Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Val	
305 310 315	

gag aac ggc aaa acc gga gtg agt ttg tcc aag gac ata acc gat gtt 1011
 Glu Asn Gly Lys Thr Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val
 320 325 330

gct ggt cga acg gtt aag aaa aac ata gca acg ctg ggt ccg ttg att 1059
 Ala Gly Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile
 335 340 345 350

ctt ccg tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag 1107
 Leu Pro Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys
 355 360 365

aaa ctt ttc aaa gac aaa atc aaa cat tat tac gtc ccg gac ttc aag 1155
 Lys Leu Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys
 370 375 380

ctt gct atc gac cat ttt tgt ata cat gcc gga ggc aaa gcc gtg att 1203
 Leu Ala Ile Asp His Phe Cys Ile His Ala Gly Gly Lys Ala Val Ile
 385 390 395

gat gtg cta gag aag aac cta ggc cta gca ccg atc gat gta gag gca 1251
 Asp Val Leu Glu Lys Asn Leu Gly Leu Ala Pro Ile Asp Val Glu Ala
 400 405 410

tca aga tca acg tta cat aga ttt gga aac act tca tct agc tca ata 1299
 Ser Arg Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile
 415 420 425 430

tgg tat gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt 1347
 Trp Tyr Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly
 435 440 445

aat aaa gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt 1395
 Asn Lys Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser
 450 455 460

gca gtt tgg gtg gct cta aac aat gtc aaa gct tcc aaa taggatcc 1442
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<210> 11

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<212> PRT

<213> Brassica sp.

<400> 11

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Ala	Tyr	Arg	Leu	Thr	Ile	Asp	Asp	Leu	His	His	Leu	Tyr	Tyr	Ser	Tyr	35	40	45
Leu	Gln	His	Asn	Leu	Ile	Thr	Ile	Ala	Pro	Leu	Phe	Ala	Phe	Thr	Val	50	55	60
Phe	Gly	Ser	Val	Leu	Tyr	Ile	Ala	Thr	Arg	Pro	Lys	Pro	Val	Tyr	Leu	65	70	75
Val	Glu	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Thr	His	Cys	Arg	Ser	Ser	Ile	85	90	95
Ser	Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Val	Arg	Lys	Ala	Asp	Pro	Ser	100	105	110
Arg	Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys	115	120	125
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly	130	135	140
Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu	145	150	155
Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr	165	170	175
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met	180	185	190
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys	195	200	205
Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	210	215	220
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His	225	230	235
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn	245	250	255
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe	260	265	270
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Arg	Asp	Arg	275	280	285
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly	290	295	300
Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Val	Glu	Asn	305	310	315
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acc aac ctt ttc aac ctt tgc ttc ttt ccg tta acg gcg atc gtc gcc 99
Thr Asn Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala
      15                   20                   25                   30

gga aaa gcc tat cgg ctt acc ata gac gat ctt cac cac tta tac tat 147
Gly Lys Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr
          35                   40                   45

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tcc tat ctc caa cac aac ctc ata acc atc gct cca ctc ttt gcc ttc	195
Ser Tyr Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe	
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acc gtt ttc ggt tcg gtt ctc tac atc gca acc cgg ccc aaa ccg gtt	243
Thr Val Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val	
65 70 75	
tac ctc gtt gag tac tca tgc tac ctt cca cca acg cat tgt aga tca	291
Tyr Leu Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser	
80 85 90	
agt atc tcc aag gtc atg gat atc ttt tat caa gta aga aaa gct gat	339
Ser Ile Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp	
95 100 105 110	
cct tct cgg aac ggc acg tgc gat gac tcg tcg tgg ctt gac ttc ttg	387
Pro Ser Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu	
115 120 125	
agg aag att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc	435
Arg Lys Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro	
130 135 140	
gag ggg ctg ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt	483
Glu Gly Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg	
145 150 155	
gaa gag acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag	531
Glu Glu Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys	
160 165 170	
aac acc aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca	579
Asn Thr Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser	
175 180 185 190	
agc atg ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act	627
Ser Met Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr	
195 200 205	
ttc aag ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt	675
Phe Lys Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly	
210 215 220	
tgt agt gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat	723
Cys Ser Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His	
225 230 235	
gtc cat aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act	771
Val His Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr	
240 245 250	

tat aac att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc	819
Tyr Asn Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys	
255 260 265 270	
ttg ttc cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga	867
Leu Phe Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly	
275 280 285	
gat cgt aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat	915
Asp Arg Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His	
290 295 300	
acc gga gct gac gac aag tct ttt cgt tgc gtg caa caa gga gac gat	963
Thr Gly Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp	
305 310 315	
gag aac ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt	1011
Glu Asn Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val	
320 325 330	
gct ggt cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att	1059
Ala Gly Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile	
335 340 345 350	
ctt ccg tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag	1107
Leu Pro Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys	
355 360 365	
aaa ctt ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa	1155
Lys Leu Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys	
370 375 380	
ctt gct att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att	1203
Leu Ala Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile	
385 390 395	
gat gtg cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca	1251
Asp Val Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala	
400 405 410	
tca aga tca acg tta cat aga ttt gga aac act tca tct agc tca ata	1299
Ser Arg Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile	
415 420 425 430	
tgg tat gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt	1347
Trp Tyr Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly	
435 440 445	
aat aaa gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt	1395
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<212> PRT
<213> Brassica sp.
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Leu	Phe	Asn	Leu	Cys	Phe	Phe	Pro	Leu	Thr	Ala	Ile	Val	Ala	Gly	Lys	
			20					25					30			
Ala	Tyr	Arg	Leu	Thr	Ile	Asp	Asp	Leu	His	His	Leu	Tyr	Tyr	Ser	Tyr	
		35					40					45				
Leu	Gln	His	Asn	Leu	Ile	Thr	Ile	Ala	Pro	Leu	Phe	Ala	Phe	Thr	Val	
	50					55					60					
Phe	Gly	Ser	Val	Leu	Tyr	Ile	Ala	Thr	Arg	Pro	Lys	Pro	Val	Tyr	Leu	
65					70				75						80	
Val	Glu	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Thr	His	Cys	Arg	Ser	Ser	Ile	
				85					90					95		
Ser	Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Val	Arg	Lys	Ala	Asp	Pro	Ser	
			100					105					110			
Arg	Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys	
		115					120					125				
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly	
	130					135					140					
Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu	
145					150					155					160	
Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr	
				165					170					175		
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met	
			180					185					190			
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys	
		195					200					205				
Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	
	210					215					220					

Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His	225	230	235	240
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn	245	250	255	
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe	260	265	270	
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg	275	280	285	
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly	290	295	300	
Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn	305	310	315	320
Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly	325	330	335	
Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro	340	345	350	
Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	Lys	Leu	355	360	365	
Phe	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala	370	375	380	
Ile	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Val	385	390	395	400
Leu	Glu	Lys	Asn	Leu	Ala	Leu	Ala	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg	405	410	415	
Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp	Tyr	420	425	430	
Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Lys	Gly	Asn	Lys	435	440	445	
Val	Trp	Gln	Ile	Ala	Leu	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Ala	Val	450	455	460	
Trp	Val	Ala	Leu	Asn	Asn	Val	Lys	Ala	Ser	Lys						465	470	475	

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<211> 623

<212> DNA

<213> Arabidopsis thaliana

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<221> CDS

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ctc ctc ctt cct ctc ctc gcc gca aca atc gct aac ctc tct tct ttc	96
Leu Leu Leu Pro Leu Leu Ala Ala Thr Ile Ala Asn Leu Ser Ser Phe	
20 25 30	
acc atc aac gac ctc tct ctc ctc tac aac aca ctc cgt ttc cat ttc	144
Thr Ile Asn Asp Leu Ser Leu Leu Tyr Asn Thr Leu Arg Phe His Phe	
35 40 45	
ctc tcc gcc aca ctc gcc acc gca ctc ttg atc tct ctc tcc acc gct	192
Leu Ser Ala Thr Leu Ala Thr Ala Leu Leu Ile Ser Leu Ser Thr Ala	
50 55 60	
tac ttc acc acc cgt cct cgc cgt gtc ttc ctc ctc gac ttc tcg tgt	240
Tyr Phe Thr Thr Arg Pro Arg Arg Val Phe Leu Leu Asp Phe Ser Cys	
65 70 75 80	
tac aaa cca gac cct tca ctg atc tgc act cgt gaa aca ttc atg gac	288
Tyr Lys Pro Asp Pro Ser Leu Ile Cys Thr Arg Glu Thr Phe Met Asp	
85 90 95	
aga tct caa cgt gta ggc atc ttc aca gaa gac aac tta gct ttc caa	336
Arg Ser Gln Arg Val Gly Ile Phe Thr Glu Asp Asn Leu Ala Phe Gln	
100 105 110	
caa aag atc ctc gaa aga tcc ggt cta ggt cag aaa act tac ttc cct	384
Gln Lys Ile Leu Glu Arg Ser Gly Leu Gly Gln Lys Thr Tyr Phe Pro	
115 120 125	
gaa gct ctt ctt cgt gtt cct cct aat cct tgt atg gaa gaa gcg aga	432
Glu Ala Leu Leu Arg Val Pro Pro Asn Pro Cys Met Glu Glu Ala Arg	
130 135 140	
aaa gag gca gaa aca gtt atg ttc gga gct att gac gcg gtt ctt gag	480
Lys Glu Ala Glu Thr Val Met Phe Gly Ala Ile Asp Ala Val Leu Glu	
145 150 155 160	
aag acc ggt gtg aaa cct aaa gat att gga atc ctt gtg gtg aat tgt	528
Lys Thr Gly Val Lys Pro Lys Asp Ile Gly Ile Leu Val Val Asn Cys	
165 170 175	
agc ttg ttt aat cca aca ccg tca ctt tct gct atg att gtg aat aag	576
Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Ile Val Asn Lys	
180 185 190	

tat aag ctt aga ggc aac att ttg agc tat aat ttc ggc ggg atg gg 623
Tyr Lys Leu Arg Gly Asn Ile Leu Ser Tyr Asn Phe Gly Gly Met Gly
195 200 205

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<212> PRT

<213> Arabidopsis thaliana

<400> 15

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20 25 30

Thr Ile Asn Asp Leu Ser Leu Leu Tyr Asn Thr Leu Arg Phe His Phe
35 40 45

Leu Ser Ala Thr Leu Ala Thr Ala Leu Leu Ile Ser Leu Ser Thr Ala
50 55 60

Tyr Phe Thr Thr Arg Pro Arg Arg Val Phe Leu Leu Asp Phe Ser Cys
65 70 75 80

Tyr Lys Pro Asp Pro Ser Leu Ile Cys Thr Arg Glu Thr Phe Met Asp
85 90 95

Arg Ser Gln Arg Val Gly Ile Phe Thr Glu Asp Asn Leu Ala Phe Gln
100 105 110

Gln Lys Ile Leu Glu Arg Ser Gly Leu Gly Gln Lys Thr Tyr Phe Pro
115 120 125

Glu Ala Leu Leu Arg Val Pro Pro Asn Pro Cys Met Glu Glu Ala Arg
130 135 140

Lys Glu Ala Glu Thr Val Met Phe Gly Ala Ile Asp Ala Val Leu Glu
145 150 155 160

Lys Thr Gly Val Lys Pro Lys Asp Ile Gly Ile Leu Val Val Asn Cys
165 170 175

Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Ile Val Asn Lys
180 185 190

Tyr Lys Leu Arg Gly Asn Ile Leu Ser Tyr Asn Phe Gly Gly Met Gly
195 200 205

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 atg ttc ctc cct cta atg gct gtt ttg ttc atg aat gtc tca ttg tta 96
 Met Phe Leu Pro Leu Met Ala Val Leu Phe Met Asn Val Ser Leu Leu
 20 25 30
 agc cta aac cat ctt cag ctc tat tac aat tcc acc gga ttc atc ttc 144
 Ser Leu Asn His Leu Gln Leu Tyr Tyr Asn Ser Thr Gly Phe Ile Phe
 35 40 45
 gtc atc act ctc gcc att gtc gga tcc att gtc ttc ttc atg tct cga 192
 Val Ile Thr Leu Ala Ile Val Gly Ser Ile Val Phe Phe Met Ser Arg
 50 55 60
 cct aga tcc atc tac ctt cta gat tac tct tgc tac ctc ccg cct tcg 240
 Pro Arg Ser Ile Tyr Leu Leu Asp Tyr Ser Cys Tyr Leu Pro Pro Ser
 65 70 75 80
 agt caa aaa gtt agc tac cag aaa ttc atg aac aac tct agt ttg att 288
 Ser Gln Lys Val Ser Tyr Gln Lys Phe Met Asn Asn Ser Ser Leu Ile
 85 90 95
 caa gat ttc agc gaa act tct ctt gag ttc cag agg aag atc ttg att 336
 Gln Asp Phe Ser Glu Thr Ser Leu Glu Phe Gln Arg Lys Ile Leu Ile
 100 105 110
 cgc tct ggt ctc ggt gaa gag act tat tta ccg gat tct att cac tct 384
 Arg Ser Gly Leu Gly Glu Glu Thr Tyr Leu Pro Asp Ser Ile His Ser
 115 120 125
 atc cct ccg cgt cct act atg gct gca gcg cgt gaa gaa gcg gag cag 432
 Ile Pro Pro Arg Pro Thr Met Ala Ala Ala Arg Glu Glu Ala Glu Gln
 130 135 140
 gta atc ttc ggt gca ctc gac aat ctt ttc gag aat aca aaa atc aat 480
 Val Ile Phe Gly Ala Leu Asp Asn Leu Phe Glu Asn Thr Lys Ile Asn
 145 150 155 160
 cct agg gag att ggt gtt ctt gtt gtg aat tgt agt ttg ttt aac ccc 528
 Pro Arg Glu Ile Gly Val Leu Val Val Asn Cys Ser Leu Phe Asn Pro
 165 170 175

acg cct tct tta tcc gcc atg att gtt aac aag tat aag ctt aga gga 576
 Thr Pro Ser Leu Ser Ala Met Ile Val Asn Lys Tyr Lys Leu Arg Gly
 180 185 190

aac att aag agc ttt aat ctc ggc ggc atg g 607
 Asn Ile Lys Ser Phe Asn Leu Gly Gly Met
 195 200

<210> 17

<211> 202

<212> PRT

<213> Arabidopsis thaliana

<400> 17

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Ser Leu Asn His Leu Gln Leu Tyr Tyr Asn Ser Thr Gly Phe Ile Phe
 35 40 45

Val Ile Thr Leu Ala Ile Val Gly Ser Ile Val Phe Phe Met Ser Arg
 50 55 60

Pro Arg Ser Ile Tyr Leu Leu Asp Tyr Ser Cys Tyr Leu Pro Pro Ser
 65 70 75 80

Ser Gln Lys Val Ser Tyr Gln Lys Phe Met Asn Asn Ser Ser Leu Ile
 85 90 95

Gln Asp Phe Ser Glu Thr Ser Leu Glu Phe Gln Arg Lys Ile Leu Ile
 100 105 110

Arg Ser Gly Leu Gly Glu Glu Thr Tyr Leu Pro Asp Ser Ile His Ser
 115 120 125

Ile Pro Pro Arg Pro Thr Met Ala Ala Ala Arg Glu Glu Ala Glu Gln
 130 135 140

Val Ile Phe Gly Ala Leu Asp Asn Leu Phe Glu Asn Thr Lys Ile Asn
 145 150 155 160

Pro Arg Glu Ile Gly Val Leu Val Val Asn Cys Ser Leu Phe Asn Pro
 165 170 175

Thr Pro Ser Leu Ser Ala Met Ile Val Asn Lys Tyr Lys Leu Arg Gly
 180 185 190

Asn Ile Lys Ser Phe Asn Leu Gly Gly Met
 195 200

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tgt ttg gtt cca tta atg gcg gtt tta gtc aca gag atc tcc cga tta 96
 Cys Leu Val Pro Leu Met Ala Val Leu Val Thr Glu Ile Ser Arg Leu
 20 25 30

aca aca gac gat ctt tac cag att tgc ctt cat ctc caa tac aat ctc 144
 Thr Thr Asp Asp Leu Tyr Gln Ile Cys Leu His Leu Gln Tyr Asn Leu
 35 40 45

gtt gct ttc atc ttt ctc tct gct tta gct atc ttt ggc tcc acc gtt 192
 Val Ala Phe Ile Phe Leu Ser Ala Leu Ala Ile Phe Gly Ser Thr Val
 50 55 60

tac atc atg agt cgt ccc aga tct gtt tat ctc gtt gat tac tct tgt 240
 Tyr Ile Met Ser Arg Pro Arg Ser Val Tyr Leu Val Asp Tyr Ser Cys
 65 70 75 80

tat ctt cct ccg gag agt ctt cag gtt aag tat cag aag ttt atg gat 288
 Tyr Leu Pro Pro Glu Ser Leu Gln Val Lys Tyr Gln Lys Phe Met Asp
 85 90 95

cat tct aag ttg att gaa gat ttc aat gag tca tct tta gag ttt cag 336
 His Ser Lys Leu Ile Glu Asp Phe Asn Glu Ser Ser Leu Glu Phe Gln
 100 105 110

agg aag att ctt gaa cgt tct ggt tta gga gaa gag act tat ctc cct 384
 Arg Lys Ile Leu Glu Arg Ser Gly Leu Gly Glu Glu Thr Tyr Leu Pro
 115 120 125

gaa gct tta cat tgt atc cct ccg agg cct acg atg atg gcg gct cgt 432
 Glu Ala Leu His Cys Ile Pro Pro Arg Pro Thr Met Met Ala Ala Arg
 130 135 140

gag gaa gct gag cag gta atg ttt ggt gct ctt gat aag ctt ttc gag 480
 Glu Glu Ala Glu Gln Val Met Phe Gly Ala Leu Asp Lys Leu Phe Glu
 145 150 155 160

aat acc aag att aac cct agg gat att ggt gtg ttg gtt gtg aat tgt 528
 Asn Thr Lys Ile Asn Pro Arg Asp Ile Gly Val Leu Val Val Asn Cys
 165 170 175

agc ttg ttt aat cct aca cct tcg ttg tca gct atg att gtt aac aag 576
 Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Ile Val Asn Lys
 180 185 190

tat aag ctt aga ggg aat gtt aag agt ttt aac ctg ggg ggc att g 622
 Tyr Lys Leu Arg Gly Asn Val Lys Ser Phe Asn Leu Gly Gly Ile
 195 200 205

<210> 19

<211> 207

<212> PRT

<213> Arabidopsis thaliana

<400> 19

Lys Leu Lys Leu Gly Tyr His Tyr Leu Ile Thr His Leu Phe Lys Leu
 1 5 10 15

Cys Leu Val Pro Leu Met Ala Val Leu Val Thr Glu Ile Ser Arg Leu
 20 25 30

Thr Thr Asp Asp Leu Tyr Gln Ile Cys Leu His Leu Gln Tyr Asn Leu
 35 40 45

Val Ala Phe Ile Phe Leu Ser Ala Leu Ala Ile Phe Gly Ser Thr Val
 50 55 60

Tyr Ile Met Ser Arg Pro Arg Ser Val Tyr Leu Val Asp Tyr Ser Cys
 65 70 75 80

Tyr Leu Pro Pro Glu Ser Leu Gln Val Lys Tyr Gln Lys Phe Met Asp
 85 90 95

His Ser Lys Leu Ile Glu Asp Phe Asn Glu Ser Ser Leu Glu Phe Gln
 100 105 110

Arg Lys Ile Leu Glu Arg Ser Gly Leu Gly Glu Glu Thr Tyr Leu Pro
 115 120 125

Glu Ala Leu His Cys Ile Pro Pro Arg Pro Thr Met Met Ala Ala Arg
 130 135 140

Glu Glu Ala Glu Gln Val Met Phe Gly Ala Leu Asp Lys Leu Phe Glu
 145 150 155 160

Asn Thr Lys Ile Asn Pro Arg Asp Ile Gly Val Leu Val Val Asn Cys
 165 170 175

Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Ile Val Asn Lys
 180 185 190

Tyr Lys Leu Arg Gly Asn Val Lys Ser Phe Asn Leu Gly Gly Ile
 195 200 205

<210> 20

<211> 625

<212> DNA

<213> Lunaria annua

<220>

<221> CDS

<222> (1) .. (624)

<400> 20

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Lys Leu Lys Leu Trp Tyr His Tyr Leu Ile Ser His Leu Phe Lys Leu	
1 5 10 15	
ttg ttg gtt cct tta atg gcg gtt ctg ttc acg aat gtc tcc cgg tta	96
Leu Leu Val Pro Leu Met Ala Val Leu Phe Thr Asn Val Ser Arg Leu	
20 25 30	
agc cta aac cag ctc tgt ctc gat ctc tct ctc cag ctc cag ttc aat	144
Ser Leu Asn Gln Leu Cys Leu Asp Leu Ser Leu Gln Leu Gln Phe Asn	
35 40 45	
ctc gtc gga ttc atc ttc ttc att acc gtc tcc att ttc gga ttc aca	192
Leu Val Gly Phe Ile Phe Phe Ile Thr Val Ser Ile Phe Gly Phe Thr	
50 55 60	
gtt atc ttc atg tcc cga cct aga tcc gtt tac ctc ctc gac tac tca	240
Val Ile Phe Met Ser Arg Pro Arg Ser Val Tyr Leu Leu Asp Tyr Ser	
65 70 75 80	
tgt tac ctc ccg ccg tcg aat ctc aaa gtt agc tac cag aca ttc atg	288
Cys Tyr Leu Pro Pro Ser Asn Leu Lys Val Ser Tyr Gln Thr Phe Met	
85 90 95	
aat cat tct aaa ctg att gaa gat ttc gac gag tcg tcg ctt gag ttc	336
Asn His Ser Lys Leu Ile Glu Asp Phe Asp Glu Ser Ser Leu Glu Phe	
100 105 110	
cag cgg aag atc ctg aag cga tcc ggt ctc ggc gaa gag act tac ctc	384
Gln Arg Lys Ile Leu Lys Arg Ser Gly Leu Gly Glu Glu Thr Tyr Leu	
115 120 125	
ccg gaa tct atc cac tgc atc ccg ccg cgt ccg act atg gcg gcg gcg	432
Pro Glu Ser Ile His Cys Ile Pro Pro Arg Pro Thr Met Ala Ala Ala	
130 135 140	

cgt gag gaa tcg gag cag gta atc ttc ggt gca ctc gac aat ctc ttc 480
 Arg Glu Glu Ser Glu Gln Val Ile Phe Gly Ala Leu Asp Asn Leu Phe
 145 150 155 160

gag aat acc aaa atc gac cct agg gag att ggt gtt gtg gtg gtg aac 528
 Glu Asn Thr Lys Ile Asp Pro Arg Glu Ile Gly Val Val Val Val Asn
 165 170 175

tgc agc ttg ttt aac ccg acg cct tct tta tcc gcc atg att gtg aac 576
 Cys Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Ile Val Asn
 180 185 190

aag tat aag ctt aga gga aac gtg aag agc ttt aat ctc ggt ggc atg g 625
 Lys Tyr Lys Leu Arg Gly Asn Val Lys Ser Phe Asn Leu Gly Gly Met
 195 200 205

<210> 21

<211> 208

<212> PRT

<213> Lunaria annua

<400> 21

Lys Leu Lys Leu Trp Tyr His Tyr Leu Ile Ser His Leu Phe Lys Leu
 1 5 10 15

Leu Leu Val Pro Leu Met Ala Val Leu Phe Thr Asn Val Ser Arg Leu
 20 25 30

Ser Leu Asn Gln Leu Cys Leu Asp Leu Ser Leu Gln Leu Gln Phe Asn
 35 40 45

Leu Val Gly Phe Ile Phe Phe Ile Thr Val Ser Ile Phe Gly Phe Thr
 50 55 60

Val Ile Phe Met Ser Arg Pro Arg Ser Val Tyr Leu Leu Asp Tyr Ser
 65 70 75 80

Cys Tyr Leu Pro Pro Ser Asn Leu Lys Val Ser Tyr Gln Thr Phe Met
 85 90 95

Asn His Ser Lys Leu Ile Glu Asp Phe Asp Glu Ser Ser Leu Glu Phe
 100 105 110

Gln Arg Lys Ile Leu Lys Arg Ser Gly Leu Gly Glu Glu Thr Tyr Leu
 115 120 125

Pro Glu Ser Ile His Cys Ile Pro Pro Arg Pro Thr Met Ala Ala Ala
 130 135 140

Arg Glu Glu Ser Glu Gln Val Ile Phe Gly Ala Leu Asp Asn Leu Phe
 145 150 155 160

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<220>  
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<222> (42) .. (1535)
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<400> 22
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Met Asp Asp Glu Ser
1 5

tta atg gcg gtt ctg ttc acg aat gtc tcc cgg tta agc cta aac cag 200
Leu Met Ala Val Leu Phe Thr Asn Val Ser Arg Leu Ser Leu Asn Gln
40 45 50

atc ttc ttc att acc gcc tcc att ttc gga ttc aca gtt atc ttc atg 296
Ile Phe Phe Ile Thr Ala Ser Ile Phe Gly Phe Thr Val Ile Phe Met
70 75 80 85

tcc	cga	cct	aga	tcc	gtt	tac	ctc	ctc	gac	tac	tca	tgt	tac	ctc	ccg	344
Ser	Arg	Pro	Arg	Ser	Val	Tyr	Leu	Leu	Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	
				90					95					100		

ncg gcg aat ctc aaa gtt agc tac cag aca ttc atg aat cat tct aaa	392
Xaa Ala Asn Leu Lys Val Ser Tyr Gln Thr Phe Met Asn His Ser Lys	
105 110 115	
ctg att gaa gat ttc gac gag tcg tcg ctt gag ttc cag cgg aag atc	440
Leu Ile Glu Asp Phe Asp Glu Ser Ser Leu Glu Phe Gln Arg Lys Ile	
120 125 130	
ctg aag cga tcc ggt ctc ggc gaa gag act tac ctc ccg gaa tct atc	488
Leu Lys Arg Ser Gly Leu Glu Glu Thr Tyr Leu Pro Glu Ser Ile	
135 140 145	
cac tgc atc ccg ccg cgt ccg act atg gcg gcg gcg cgt gag gaa tcg	536
His Cys Ile Pro Pro Arg Pro Thr Met Ala Ala Ala Arg Glu Glu Ser	
150 155 160 165	
gag cag gta atc ttc ggt gca ctc gac aat ctc ttc gag aat acc aaa	584
Glu Gln Val Ile Phe Gly Ala Leu Asp Asn Leu Phe Glu Asn Thr Lys	
170 175 180	
atc gac cct agg gag att ggt gtt gtg gtg gtg aac tgc agc ttg ttt	632
Ile Asp Pro Arg Glu Ile Gly Val Val Val Val Asn Cys Ser Leu Phe	
185 190 195	
aac ccg acg cct tct tta tcc gcc atg att gtg aac aag tat aag ctt	680
Asn Pro Thr Pro Ser Leu Ser Ala Met Ile Val Asn Lys Tyr Lys Leu	
200 205 210	
aga gga aac gtg aag agc ttt aac ctc gga gga atg gga tgt agg gct	728
Arg Gly Asn Val Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Arg Ala	
215 220 225	
ggt gtc atc gcc gtt gat ctc gct aat gac att tta cag ctc cat aga	776
Gly Val Ile Ala Val Asp Leu Ala Asn Asp Ile Leu Gln Leu His Arg	
230 235 240 245	
aac aca tta gct ctt gtg gtt agc aca gag aac atc act cag aat tgg	824
Asn Thr Leu Ala Leu Val Ser Thr Glu Asn Ile Thr Gln Asn Trp	
250 255 260	
tac ttt ggt aac aac aaa gca atg ttg att cct aat tgc ttg ttt agg	872
Tyr Phe Gly Asn Asn Lys Ala Met Leu Ile Pro Asn Cys Leu Phe Arg	
265 270 275	
gtt ggt gga tcc gcg gtt ctg ctt tcg aac aag cct cgt gat cga aaa	920
Val Gly Gly Ser Ala Val Leu Leu Ser Asn Lys Pro Arg Asp Arg Lys	
280 285 290	
cga tcc aag tat aaa ctt gtt cac acg gta cgg act cat aaa gga tct	968
Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Lys Gly Ser	
295 300 305	

gat gag aaa gca ttc aac tgt gtg tac caa gaa caa gac gag gac ttg	1016
Asp Glu Lys Ala Phe Asn Cys Val Tyr Gln Glu Gln Asp Glu Asp Leu	
310 315 320 325	
aaa acc gga gtt tct ttg tct aaa gac cta atg tct ata gct gga gaa	1064
Lys Thr Gly Val Ser Leu Ser Lys Asp Leu Met Ser Ile Ala Gly Glu	
330 335 340	
gct cta aag aca aat atc acc act ttg ggt cct ctg gtt ctt cca ata	1112
Ala Leu Lys Thr Asn Ile Thr Thr Leu Gly Pro Leu Val Leu Pro Ile	
345 350 355	
agc gag cag att ctg ttc att gcg act ttt gtt gca aag aga ttg ttc	1160
Ser Glu Gln Ile Leu Phe Ile Ala Thr Phe Val Ala Lys Arg Leu Phe	
360 365 370	
agt gcc aag aag aag aag aag aag cct tac ata ccg gat ttc aag ctt	1208
Ser Ala Lys Lys Lys Lys Lys Lys Pro Tyr Ile Pro Asp Phe Lys Leu	
375 380 385	
gcc ttt gat cat ttc tgt att cac gca gga ggt aga gcc gtg atc gat	1256
Ala Phe Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp	
390 395 400 405	
gaa cta gag aag agt tta aag cta ttg cca aaa cat gtg gag gct tct	1304
Glu Leu Glu Lys Ser Leu Lys Leu Leu Pro Lys His Val Glu Ala Ser	
410 415 420	
aga atg aca ttg cat aga ttt gga aac act tca tcg agc tct att tgg	1352
Arg Met Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp	
425 430 435	
tat gaa tta gct tac aca gaa gct aaa gga aga atg aga aaa ggg aat	1400
Tyr Glu Leu Ala Tyr Thr Glu Ala Lys Gly Arg Met Arg Lys Gly Asn	
440 445 450	
cga gtt tgg cag att gct ttt gga agc ggc ttt aag tgt aac agc gcg	1448
Arg Val Trp Gln Ile Ala Phe Gly Ser Gly Phe Lys Cys Asn Ser Ala	
455 460 465	
gtt tgg gtg gct ctt cgt gat gtc gag ccc tcg gtt aac aat cct tgg	1496
Val Trp Val Ala Leu Arg Asp Val Glu Pro Ser Val Asn Asn Pro Trp	
470 475 480 485	
gaa cat tgc atc cat aga tat ccg gtt aag atc gat ctc tgatttcagc	1545
Glu His Cys Ile His Arg Tyr Pro Val Lys Ile Asp Leu	
490 495	
ttaaccggta aaattggtct gtacatatat ttaccactga gtaaagacat cagttaatga	1605
tttgttggtta ctcaattggg ctaagtgtat tattatatgt gttgtatata ataaaggtag	1665
aacgtaaatt tactaagaaa aaaaaaaaaa aaaaaaaaaa	1704

<210> 23
 <211> 498
 <212> PRT
 <213> *Lunaria annua*

<220>
 <221> MOD_RES
 <222> (102)
 <223> Variable amino acid

<400> 23
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 1 5 10 15
 Lys Tyr Val Lys Leu Gly Tyr His Tyr Leu Ile Ser His Leu Phe Lys
 20 25 30
 Leu Leu Leu Val Pro Leu Met Ala Val Leu Phe Thr Asn Val Ser Arg
 35 40 45
 Leu Ser Leu Asn Gln Leu Cys Leu Asp Leu Ser Leu Gln Leu Gln Phe
 50 55 60
 Asn Leu Val Gly Phe Ile Phe Phe Ile Thr Ala Ser Ile Phe Gly Phe
 65 70 75 80
 Thr Val Ile Phe Met Ser Arg Pro Arg Ser Val Tyr Leu Leu Asp Tyr
 85 90 95
 Ser Cys Tyr Leu Pro Xaa Ala Asn Leu Lys Val Ser Tyr Gln Thr Phe
 100 105 110
 Met Asn His Ser Lys Leu Ile Glu Asp Phe Asp Glu Ser Ser Leu Glu
 115 120 125
 Phe Gln Arg Lys Ile Leu Lys Arg Ser Gly Leu Gly Glu Glu Thr Tyr
 130 135 140
 Leu Pro Glu Ser Ile His Cys Ile Pro Pro Arg Pro Thr Met Ala Ala
 145 150 155 160
 Ala Arg Glu Glu Ser Glu Gln Val Ile Phe Gly Ala Leu Asp Asn Leu
 165 170 175
 Phe Glu Asn Thr Lys Ile Asp Pro Arg Glu Ile Gly Val Val Val Val
 180 185 190
 Asn Cys Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Ile Val
 195 200 205
 Asn Lys Tyr Lys Leu Arg Gly Asn Val Lys Ser Phe Asn Leu Gly Gly
 210 215 220

Met Gly Cys Arg Ala Gly Val Ile Ala Val Asp Leu Ala Asn Asp Ile
 225 230 235 240
 Leu Gln Leu His Arg Asn Thr Leu Ala Leu Val Val Ser Thr Glu Asn
 245 250 255
 Ile Thr Gln Asn Trp Tyr Phe Gly Asn Asn Lys Ala Met Leu Ile Pro
 260 265 270
 Asn Cys Leu Phe Arg Val Gly Gly Ser Ala Val Leu Leu Ser Asn Lys
 275 280 285
 Pro Arg Asp Arg Lys Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg
 290 295 300
 Thr His Lys Gly Ser Asp Glu Lys Ala Phe Asn Cys Val Tyr Gln Glu
 305 310 315 320
 Gln Asp Glu Asp Leu Lys Thr Gly Val Ser Leu Ser Lys Asp Leu Met
 325 330 335
 Ser Ile Ala Gly Glu Ala Leu Lys Thr Asn Ile Thr Thr Leu Gly Pro
 340 345 350
 Leu Val Leu Pro Ile Ser Glu Gln Ile Leu Phe Ile Ala Thr Phe Val
 355 360 365
 Ala Lys Arg Leu Phe Ser Ala Lys Lys Lys Lys Lys Lys Pro Tyr Ile
 370 375 380
 Pro Asp Phe Lys Leu Ala Phe Asp His Phe Cys Ile His Ala Gly Gly
 385 390 395 400
 Arg Ala Val Ile Asp Glu Leu Glu Lys Ser Leu Lys Leu Leu Pro Lys
 405 410 415
 His Val Glu Ala Ser Arg Met Thr Leu His Arg Phe Gly Asn Thr Ser
 420 425 430
 Ser Ser Ser Ile Trp Tyr Glu Leu Ala Tyr Thr Glu Ala Lys Gly Arg
 435 440 445
 Met Arg Lys Gly Asn Arg Val Trp Gln Ile Ala Phe Gly Ser Gly Phe
 450 455 460
 Lys Cys Asn Ser Ala Val Trp Val Ala Leu Arg Asp Val Glu Pro Ser
 465 470 475 480
 Val Asn Asn Pro Trp Glu His Cys Ile His Arg Tyr Pro Val Lys Ile
 485 490 495
 Asp Leu

<210> 24
 <211> 1664
 <212> DNA
 <213> Lunaria annua

<220>
 <221> CDS
 <222> (3)..(1517)

<220>
 <221> modified_base
 <222> (155)
 <223> a, c, t, or g

<220>
 <221> modified_base
 <222> (217)
 <223> a, c, t, or g

<400> 24
 ca atg acg tct gtg aac gta aaa ctc ctt tac cat tac gtc ata acc 47
 Met Thr Ser Val Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr
 1 5 10 15
 aac ttt ttc aac ctc tgt ttc ttc cca ctg acg ggg atc ctc gcc gga 95
 Asn Phe Phe Asn Leu Cys Phe Phe Pro Leu Thr Gly Ile Leu Ala Gly
 20 25 30
 aaa ggc tct cgt ctt acc aca aac gat ctc cac cac ttc tat tca tat 143
 Lys Gly Ser Arg Leu Thr Thr Asn Asp Leu His His Phe Tyr Ser Tyr
 35 40 45
 ctc caa cac aan ctt ata acc tta acc cta ctc ttt ggc ttc acc gtt 191
 Leu Gln His Xaa Leu Ile Thr Leu Thr Leu Leu Phe Gly Phe Thr Val
 50 55 60
 ttt ggt tcg gtt ctc tac ttc gta anc cga ccc aaa ccg gtt tac ctc 239
 Phe Gly Ser Val Leu Tyr Phe Val Xaa Arg Pro Lys Pro Val Tyr Leu
 65 70 75
 gtt gac tac tcc tgc tac ctt cca cca caa cat ctt agc gct ggt atc 287
 Val Asp Tyr Ser Cys Tyr Leu Pro Pro Gln His Leu Ser Ala Gly Ile
 80 85 90 95
 tct aag acc atg gaa atc ttt tat caa ata aga aaa tct gat cct tta 335
 Ser Lys Thr Met Glu Ile Phe Tyr Gln Ile Arg Lys Ser Asp Pro Leu
 100 105 110
 cga aac gtg gca tta gat gat tgc tct tct ctt gat ttc ttg aga aag 383
 Arg Asn Val Ala Leu Asp Asp Ser Ser Ser Leu Asp Phe Leu Arg Lys
 115 120 125

att caa gag cgt tca ggt cta ggc gat gaa acc tac ggc ccc gag gga Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Gly Pro Glu Gly 130 135 140	431
ctg ttt gag att cct ccg agg aag aat tta gcg tcg gcg cgt gaa gag Leu Phe Glu Ile Pro Pro Arg Lys Asn Leu Ala Ser Ala Arg Glu Glu 145 150 155	479
acg gag caa gta atc aac ggt gcg cta aaa aat cta ttc gag aac aac Thr Glu Gln Val Ile Asn Gly Ala Leu Lys Asn Leu Phe Glu Asn Asn 160 165 170 175	527
aaa gtt aac cct aaa gag att ggt ata ctt gtg gtg aac tca agc atg Lys Val Asn Pro Lys Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met 180 185 190	575
ttt aat ccg act cct tcg tta tcc gcg atg gta gtt aat act tcc aag Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Ser Lys 195 200 205	623
ctc cga agc aac atc aaa agc ttt aat ctt gga gga atg ggt tgc agt Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser 210 215 220	671
gct ggt gtt atc gcc att gat cta gct aaa gac ttg ttg cat gtt cat Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His 225 230 235	719
aaa aac aca tat gct ctt gtg gtg agc aca gag aac atc act caa aac Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Asn 240 245 250 255	767
att tat acc ggt gat aac aga tcc atg atg gtt tcg aat tgc ttg ttc Ile Tyr Thr Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe 260 265 270	815
cgt gtc ggt ggg gca gcg att ctg ctc tcc aac aag ccg ggg gat cga Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg 275 280 285	863
aga cgg tcc aag tac aag cta gct cac acg gtt cga acg cat acc gga Arg Arg Ser Lys Tyr Lys Leu Ala His Thr Val Arg Thr His Thr Gly 290 295 300	911
gct gac gac aag tct ttt gga tgt gtg cgg caa gaa gaa gat gat agc Ala Asp Asp Lys Ser Phe Gly Cys Val Arg Gln Glu Glu Asp Asp Ser 305 310 315	959
ggt aaa acc gga gtt agt ttg tca aaa gac ata acc gtt gtt gcc ggg Gly Lys Thr Gly Val Ser Leu Ser Lys Asp Ile Thr Val Val Ala Gly 320 325 330 335	1007

ata acg gtt cag aaa aac ata aca aca ttg ggt ccg ttg gtt ctt cct	1055
Ile Thr Val Gln Lys Asn Ile Thr Thr Leu Gly Pro Leu Val Leu Pro	
340 345 350	
ctg agc gaa aaa atc ctt ttt gtc gtt aca ttc gta gcc aag aaa cta	1103
Leu Ser Glu Lys Ile Leu Phe Val Val Thr Phe Val Ala Lys Lys Leu	
355 360 365	
tta aaa gat aag atc aaa cac tat tac gtg ccg gat ttc aaa ctt gca	1151
Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala	
370 375 380	
gta gat cat ttc tgt att cat gcg gga ggt aga gcc gtg ata gat gtg	1199
Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val	
385 390 395	
tta gag aag aac tta ggg cta tcg ccg ata gat gtg gag gca tca aga	1247
Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg	
400 405 410 415	
tca aca tta cat aga ttt ggg aat aca tcg tct agt tca att tgg tat	1295
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr	
420 425 430	
gaa tta gca tac ata gag cca aaa gga agg atg aag aaa ggt aat aaa	1343
Glu Leu Ala Tyr Ile Glu Pro Lys Gly Arg Met Lys Lys Gly Asn Lys	
435 440 445	
gct tgc caa ata gct ggt ggg tca ggt ttt aag tgt aat agt gcg gtt	1391
Ala Cys Gln Ile Ala Gly Gly Ser Gly Phe Lys Cys Asn Ser Ala Val	
450 455 460	
tgg gtc gct tta cgc aat gtc gag gct tca gct aat agt cct tgg gaa	1439
Trp Val Ala Leu Arg Asn Val Glu Ala Ser Ala Asn Ser Pro Trp Glu	
465 470 475	
cat tgc att cac aaa tat ccg gtt caa atg tat tct ggt tca tca aag	1487
His Cys Ile His Lys Tyr Pro Val Gln Met Tyr Ser Gly Ser Ser Lys	
480 485 490 495	
tca gag act cct gtc caa aac ggt cgg tcc taatttatgt atctcaaatg	1537
Ser Glu Thr Pro Val Gln Asn Gly Arg Ser	
500 505	
atgttggtcca ctttctcttt ttttttttct ttttttagtt ataatttaaat gggttacgatg	1597
ttttgtctag gtcgttataa ataaagaata catgggtggt actagtataa aaaaaaaaaa	1657
aaaaaaaa	1664

<210> 25
 <211> 505
 <212> PRT
 <213> Lunaria annua

<220>
 <221> MOD_RES
 <222> (51)
 <223> Variable amino acid

<220>
 <221> MOD_RES
 <222> (72)
 <223> Variable amino acid

<400> 25
 Met Thr Ser Val Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn
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 Phe Phe Asn Leu Cys Phe Phe Pro Leu Thr Gly Ile Leu Ala Gly Lys
 20 25 30
 Gly Ser Arg Leu Thr Thr Asn Asp Leu His His Phe Tyr Ser Tyr Leu
 35 40 45
 Gln His Xaa Leu Ile Thr Leu Thr Leu Leu Phe Gly Phe Thr Val Phe
 50 55 60
 Gly Ser Val Leu Tyr Phe Val Xaa Arg Pro Lys Pro Val Tyr Leu Val
 65 70 75 80
 Asp Tyr Ser Cys Tyr Leu Pro Pro Gln His Leu Ser Ala Gly Ile Ser
 85 90 95
 Lys Thr Met Glu Ile Phe Tyr Gln Ile Arg Lys Ser Asp Pro Leu Arg
 100 105 110
 Asn Val Ala Leu Asp Asp Ser Ser Ser Leu Asp Phe Leu Arg Lys Ile
 115 120 125
 Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Gly Pro Glu Gly Leu
 130 135 140
 Phe Glu Ile Pro Pro Arg Lys Asn Leu Ala Ser Ala Arg Glu Glu Thr
 145 150 155 160
 Glu Gln Val Ile Asn Gly Ala Leu Lys Asn Leu Phe Glu Asn Asn Lys
 165 170 175
 Val Asn Pro Lys Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met Phe
 180 185 190
 Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Ser Lys Leu
 195 200 205

Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser Ala
 210 215 220
 Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His Lys
 225 230 235 240
 Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Asn Ile
 245 250 255
 Tyr Thr Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe Arg
 260 265 270
 Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg Arg
 275 280 285
 Arg Ser Lys Tyr Lys Leu Ala His Thr Val Arg Thr His Thr Gly Ala
 290 295 300
 Asp Asp Lys Ser Phe Gly Cys Val Arg Gln Glu Glu Asp Asp Ser Gly
 305 310 315 320
 Lys Thr Gly Val Ser Leu Ser Lys Asp Ile Thr Val Val Ala Gly Ile
 325 330 335
 Thr Val Gln Lys Asn Ile Thr Thr Leu Gly Pro Leu Val Leu Pro Leu
 340 345 350
 Ser Glu Lys Ile Leu Phe Val Val Thr Phe Val Ala Lys Lys Leu Leu
 355 360 365
 Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala Val
 370 375 380
 Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val Leu
 385 390 395 400
 Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg Ser
 405 410 415
 Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr Glu
 420 425 430
 Leu Ala Tyr Ile Glu Pro Lys Gly Arg Met Lys Lys Gly Asn Lys Ala
 435 440 445
 Cys Gln Ile Ala Gly Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp
 450 455 460
 Val Ala Leu Arg Asn Val Glu Ala Ser Ala Asn Ser Pro Trp Glu His
 465 470 475 480
 Cys Ile His Lys Tyr Pro Val Gln Met Tyr Ser Gly Ser Ser Lys Ser
 485 490 495

Glu Thr Pro Val Gln Asn Gly Arg Ser
500 505

<210> 26
<211> 1732
<212> DNA
<213> Lunaria annua

<220>
<221> CDS
<222> (19)..(1611)

<400> 26
ctttcttctt cccaaca atg acc cat aac caa aac caa cct cac cgg gca 51
Met Thr His Asn Gln Asn Gln Pro His Arg Ala
1 5 10

gtt ccg gtt cac gtt aca aac tcc gat caa aac caa aac caa aac caa 99
Val Pro Val His Val Thr Asn Ser Asp Gln Asn Gln Asn Gln Asn Gln
15 20 25

aac aat ctc cca aat ttt ctc tta tct gtt cgg ctc aaa tat gta aaa 147
Asn Asn Leu Pro Asn Phe Leu Leu Ser Val Arg Leu Lys Tyr Val Lys
30 35 40

ctt ggg tac cat tac cta atc tcc aac ggt ctc tac atc ctc ctc ctc 195
Leu Gly Tyr His Tyr Leu Ile Ser Asn Gly Leu Tyr Ile Leu Leu Leu
45 50 55

cct ctc ctc ggc ggc aca atc gta aaa ctc tct tcc ttc aca ctc aac 243
Pro Leu Leu Gly Gly Thr Ile Val Lys Leu Ser Ser Phe Thr Leu Asn
60 65 70 75

gaa ctc tct ctc ctc tac aac cac ctc cgt ttt cat ttc ctc tcc gcc 291
Glu Leu Ser Leu Leu Tyr Asn His Leu Arg Phe His Phe Leu Ser Ala
80 85 90

aca ctc gct acc gga ctc tta atc tct ctc tcc acc gcc tac ttc acc 339
Thr Leu Ala Thr Gly Leu Leu Ile Ser Leu Ser Thr Ala Tyr Phe Thr
95 100 105

acc cgt cct cgt cat gtc ttc ctc ctc gac ttc tca tgc tac aaa cct 387
Thr Arg Pro Arg His Val Phe Leu Leu Asp Phe Ser Cys Tyr Lys Pro
110 115 120

gac cct tcc tta ata tgc act cgt gaa aca ttc atg gac cga tct caa 435
Asp Pro Ser Leu Ile Cys Thr Arg Glu Thr Phe Met Asp Arg Ser Gln
125 130 135

cgt	gta	ggg	atc	ttc	aca	gaa	gac	aac	ctc	gct	ttt	caa	caa	aag	atc	483
Arg	Val	Gly	Ile	Phe	Thr	Glu	Asp	Asn	Leu	Ala	Phe	Gln	Gln	Lys	Ile	
140					145					150					155	
ctc	gaa	aga	tcc	ggg	ctt	ggg	cag	aaa	act	tac	ttc	cct	gaa	gct	ctt	531
Leu	Glu	Arg	Ser	Gly	Leu	Gly	Gln	Lys	Thr	Tyr	Phe	Pro	Glu	Ala	Leu	
				160					165						170	
ctt	cgt	gtt	cct	ccc	aat	cct	tgt	atg	gaa	gaa	gcg	aga	aaa	gaa	gca	579
Leu	Arg	Val	Pro	Pro	Asn	Pro	Cys	Met	Glu	Glu	Ala	Arg	Lys	Glu	Ala	
			175					180					185			
gag	act	gtt	atg	ttc	gga	gct	ata	gac	tct	gtt	ctt	gag	aaa	acc	ggg	627
Glu	Thr	Val	Met	Phe	Gly	Ala	Ile	Asp	Ser	Val	Leu	Glu	Lys	Thr	Gly	
		190						195				200				
gtg	aaa	cct	aaa	gat	atc	gga	atc	ctt	gtc	gtg	aat	tgt	agt	ttg	ttt	675
Val	Lys	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Cys	Ser	Leu	Phe	
	205					210					215					
aat	ccg	acg	ccg	tca	ctt	tcc	gcc	atg	att	gtg	aat	aag	tat	aag	ctt	723
Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Ile	Val	Asn	Lys	Tyr	Lys	Leu	
220					225					230					235	
aga	gga	aac	att	ttg	agc	tat	aat	ctc	ggg	gga	atg	ggg	tgt	agt	gct	771
Arg	Gly	Asn	Ile	Leu	Ser	Tyr	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	Ala	
				240					245					250		
gga	ctt	atc	tcc	att	gat	ctc	gct	aaa	cag	ctt	ctt	cag	gtc	caa	cca	819
Gly	Leu	Ile	Ser	Ile	Asp	Leu	Ala	Lys	Gln	Leu	Leu	Gln	Val	Gln	Pro	
			255					260					265			
aac	tca	tac	gca	cta	gtg	gtg	agc	aca	gag	aac	ata	acc	tta	aac	tg	867
Asn	Ser	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Leu	Asn	Trp	
		270					275					280				
tac	tta	ggc	aac	gac	cga	tca	atg	ctt	ctc	tct	aac	tgc	atc	ttc	cgt	915
Tyr	Leu	Gly	Asn	Asp	Arg	Ser	Met	Leu	Leu	Ser	Asn	Cys	Ile	Phe	Arg	
	285					290					295					
atg	gga	gga	gcc	gcc	gta	ctt	ctc	tca	aac	cgt	tcc	tcc	gat	cgc	acc	963
Met	Gly	Gly	Ala	Ala	Val	Leu	Leu	Ser	Asn	Arg	Ser	Ser	Asp	Arg	Thr	
300					305					310					315	
cgt	tca	aaa	tat	cag	ctc	atc	cac	ccc	gtc	cgt	acc	cac	aaa	gga	gcc	1011
Arg	Ser	Lys	Tyr	Gln	Leu	Ile	His	Pro	Val	Arg	Thr	His	Lys	Gly	Ala	
				320					325					330		
aac	gac	aac	gca	ttt	ggc	tgc	gtt	tac	caa	cga	gaa	gac	aac	aac	gaa	1059
Asn	Asp	Asn	Ala	Phe	Gly	Cys	Val	Tyr	Gln	Arg	Glu	Asp	Asn	Asn	Glu	
			335					340					345			

gaa gaa acc gcc aaa atc gga gtc tca ctc tct aaa aac cta atg gca 1107
 Glu Glu Thr Ala Lys Ile Gly Val Ser Leu Ser Lys Asn Leu Met Ala
 350 355 360

ata gcc gga gaa gct ctc aag aca aac ata aca aca ctc gga cca cta 1155
 Ile Ala Gly Glu Ala Leu Lys Thr Asn Ile Thr Thr Leu Gly Pro Leu
 365 370 375

gtc tta cca atg tcc gaa cag att ctg ttt ttc cca aca ctc gtg gct 1203
 Val Leu Pro Met Ser Glu Gln Ile Leu Phe Phe Pro Thr Leu Val Ala
 380 385 390 395

cga aaa atc ttc aaa gtc aag aaa ata aag cct tac ata ccc gat ttc 1251
 Arg Lys Ile Phe Lys Val Lys Lys Ile Lys Pro Tyr Ile Pro Asp Phe
 400 405 410

aag cta gct ttc gag cat ttc tgc atc cat gcg gga ggt aga gca gtg 1299
 Lys Leu Ala Phe Glu His Phe Cys Ile His Ala Gly Gly Arg Ala Val
 415 420 425

ctt gat gag ata gag aag aat ttg gat tta tca gag tgg cat atg gaa 1347
 Leu Asp Glu Ile Glu Lys Asn Leu Asp Leu Ser Glu Trp His Met Glu
 430 435 440

cca tcg agg atg act tta aac cgg ttt ggt aat act tcg agt agc tca 1395
 Pro Ser Arg Met Thr Leu Asn Arg Phe Gly Asn Thr Ser Ser Ser Ser
 445 450 455

ctt tgg tat gaa ctt gcg tat agt gaa gct aaa ggg agg att aag aga 1443
 Leu Trp Tyr Glu Leu Ala Tyr Ser Glu Ala Lys Gly Arg Ile Lys Arg
 460 465 470 475

gga gat agg act tgc caa att gcg ttt gga tcg gga ttt aag tgt aat 1491
 Gly Asp Arg Thr Cys Gln Ile Ala Phe Gly Ser Gly Phe Lys Cys Asn
 480 485 490

agt gcg gtt tgg aaa gct ttg aga acc att gat cct att gat gag aag 1539
 Ser Ala Val Trp Lys Ala Leu Arg Thr Ile Asp Pro Ile Asp Glu Lys
 495 500 505

aag aat cca tgg agt gat gag att cat gag ttt cca gtt tct gtt cct 1587
 Lys Asn Pro Trp Ser Asp Glu Ile His Glu Phe Pro Val Ser Val Pro
 510 515 520

agg atc act cca gtt act tct aac tagtggttttt tttttggggtc caactagggga 1641
 Arg Ile Thr Pro Val Thr Ser Asn
 525 530

taatatttgt tatgggttttg ttcttacgta cgtacttttaa gtgatttagt ctaaaaaataa 1701

attggtttca taaaaaaaaa aaaaaaaaaa a 1732

<210> 27

<211> 531

<212> PRT

<213> Lunaria annua

<400> 27

Met Thr His Asn Gln Asn Gln Pro His Arg Ala Val Pro Val His Val
 1 5 10 15

Thr Asn Ser Asp Gln Asn Gln Asn Gln Asn Gln Asn Asn Leu Pro Asn
 20 25 30

Phe Leu Leu Ser Val Arg Leu Lys Tyr Val Lys Leu Gly Tyr His Tyr
 35 40 45

Leu Ile Ser Asn Gly Leu Tyr Ile Leu Leu Leu Pro Leu Leu Gly Gly
 50 55 60

Thr Ile Val Lys Leu Ser Ser Phe Thr Leu Asn Glu Leu Ser Leu Leu
 65 70 75 80

Tyr Asn His Leu Arg Phe His Phe Leu Ser Ala Thr Leu Ala Thr Gly
 85 90 95

Leu Leu Ile Ser Leu Ser Thr Ala Tyr Phe Thr Thr Arg Pro Arg His
 100 105 110

Val Phe Leu Leu Asp Phe Ser Cys Tyr Lys Pro Asp Pro Ser Leu Ile
 115 120 125

Cys Thr Arg Glu Thr Phe Met Asp Arg Ser Gln Arg Val Gly Ile Phe
 130 135 140

Thr Glu Asp Asn Leu Ala Phe Gln Gln Lys Ile Leu Glu Arg Ser Gly
 145 150 155 160

Leu Gly Gln Lys Thr Tyr Phe Pro Glu Ala Leu Leu Arg Val Pro Pro
 165 170 175

Asn Pro Cys Met Glu Glu Ala Arg Lys Glu Ala Glu Thr Val Met Phe
 180 185 190

Gly Ala Ile Asp Ser Val Leu Glu Lys Thr Gly Val Lys Pro Lys Asp
 195 200 205

Ile Gly Ile Leu Val Val Asn Cys Ser Leu Phe Asn Pro Thr Pro Ser
 210 215 220

Leu Ser Ala Met Ile Val Asn Lys Tyr Lys Leu Arg Gly Asn Ile Leu
 225 230 235 240

Ser Tyr Asn Leu Gly Gly Met Gly Cys Ser Ala Gly Leu Ile Ser Ile
 245 250 255

Asp Leu Ala Lys Gln Leu Leu Gln Val Gln Pro Asn Ser Tyr Ala Leu
 260 265 270
 Val Val Ser Thr Glu Asn Ile Thr Leu Asn Trp Tyr Leu Gly Asn Asp
 275 280 285
 Arg Ser Met Leu Leu Ser Asn Cys Ile Phe Arg Met Gly Gly Ala Ala
 290 295 300
 Val Leu Leu Ser Asn Arg Ser Ser Asp Arg Thr Arg Ser Lys Tyr Gln
 305 310 315 320
 Leu Ile His Pro Val Arg Thr His Lys Gly Ala Asn Asp Asn Ala Phe
 325 330 335
 Gly Cys Val Tyr Gln Arg Glu Asp Asn Asn Glu Glu Glu Thr Ala Lys
 340 345 350
 Ile Gly Val Ser Leu Ser Lys Asn Leu Met Ala Ile Ala Gly Glu Ala
 355 360 365
 Leu Lys Thr Asn Ile Thr Thr Leu Gly Pro Leu Val Leu Pro Met Ser
 370 375 380
 Glu Gln Ile Leu Phe Phe Pro Thr Leu Val Ala Arg Lys Ile Phe Lys
 385 390 395 400
 Val Lys Lys Ile Lys Pro Tyr Ile Pro Asp Phe Lys Leu Ala Phe Glu
 405 410 415
 His Phe Cys Ile His Ala Gly Gly Arg Ala Val Leu Asp Glu Ile Glu
 420 425 430
 Lys Asn Leu Asp Leu Ser Glu Trp His Met Glu Pro Ser Arg Met Thr
 435 440 445
 Leu Asn Arg Phe Gly Asn Thr Ser Ser Ser Ser Leu Trp Tyr Glu Leu
 450 455 460
 Ala Tyr Ser Glu Ala Lys Gly Arg Ile Lys Arg Gly Asp Arg Thr Cys
 465 470 475 480
 Gln Ile Ala Phe Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp Lys
 485 490 495
 Ala Leu Arg Thr Ile Asp Pro Ile Asp Glu Lys Lys Asn Pro Trp Ser
 500 505 510
 Asp Glu Ile His Glu Phe Pro Val Ser Val Pro Arg Ile Thr Pro Val
 515 520 525
 Thr Ser Asn
 530

<210> 28
 <211> 622
 <212> DNA
 <213> Tropaeolum majus

<220>
 <221> CDS
 <222> (1)..(621)

<400> 28
 aag ctt aaa cta gta tac cat tac ttg atc tcc aac gcc atg tat ttg 48
 Lys Leu Lys Leu Val Tyr His Tyr Leu Ile Ser Asn Ala Met Tyr Leu
 1 5 10 15

tta atg gtg ccg ctt cta gca gta gcc ttt gct cat ctc tcc acg ttg 96
 Leu Met Val Pro Leu Leu Ala Val Ala Phe Ala His Leu Ser Thr Leu
 20 25 30

acg att caa gat ctg gtt cat ctt tgg gaa cag ctt aag ttc aat tta 144
 Thr Ile Gln Asp Leu Val His Leu Trp Glu Gln Leu Lys Phe Asn Leu
 35 40 45

ctg tca gta act ctc tgc tcg agc ctt atg gtg ttt tta ggg act ctg 192
 Leu Ser Val Thr Leu Cys Ser Ser Leu Met Val Phe Leu Gly Thr Leu
 50 55 60

tat ttc atg agc cga ccg acg aag att tac ttg gtg gat ttc tct tgt 240
 Tyr Phe Met Ser Arg Pro Thr Lys Ile Tyr Leu Val Asp Phe Ser Cys
 65 70 75 80

tac aag ccg gaa aaa gag cgt ata tgc acg aga gag att ttc tat gag 288
 Tyr Lys Pro Glu Lys Glu Arg Ile Cys Thr Arg Glu Ile Phe Tyr Glu
 85 90 95

aga tcg aaa cta act ggg aat ttt acc gat gat aat tta act ttc caa 336
 Arg Ser Lys Leu Thr Gly Asn Phe Thr Asp Asp Asn Leu Thr Phe Gln
 100 105 110

aag aaa att atc gaa aga tct gga tta ggt cag aac acg tac tta cct 384
 Lys Lys Ile Ile Glu Arg Ser Gly Leu Gly Gln Asn Thr Tyr Leu Pro
 115 120 125

gag gcc gtt cta cgg gtt ccg ccc aat ccg tgt atg gcg gag gct aga 432
 Glu Ala Val Leu Arg Val Pro Pro Asn Pro Cys Met Ala Glu Ala Arg
 130 135 140

aag gag gct gag atg gtt atg ttc ggt gcg atc gat gaa ttg ttg gag 480
 Lys Glu Ala Glu Met Val Met Phe Gly Ala Ile Asp Glu Leu Leu Glu
 145 150 155 160

aaa acc ggg gtt aaa cct aag gat atc ggt att ctt gtg gtg aat tgc 528
 Lys Thr Gly Val Lys Pro Lys Asp Ile Gly Ile Leu Val Val Asn Cys
 165 170 175

agc ttg ttc aat ccg acg ccg tct ctg tcc gca atg gtg gtt aat cgg 576
 Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Arg
 180 185 190

tac aag ctt aga ggg aat atc ata agt tat aac ctt ggc ggg atg g 622
 Tyr Lys Leu Arg Gly Asn Ile Ile Ser Tyr Asn Leu Gly Gly Met
 195 200 205

<210> 29

<211> 207

<212> PRT

<213> Tropaeolum majus

<400> 29

Lys Leu Lys Leu Val Tyr His Tyr Leu Ile Ser Asn Ala Met Tyr Leu
 1 5 10 15

Leu Met Val Pro Leu Leu Ala Val Ala Phe Ala His Leu Ser Thr Leu
 20 25 30

Thr Ile Gln Asp Leu Val His Leu Trp Glu Gln Leu Lys Phe Asn Leu
 35 40 45

Leu Ser Val Thr Leu Cys Ser Ser Leu Met Val Phe Leu Gly Thr Leu
 50 55 60

Tyr Phe Met Ser Arg Pro Thr Lys Ile Tyr Leu Val Asp Phe Ser Cys
 65 70 75 80

Tyr Lys Pro Glu Lys Glu Arg Ile Cys Thr Arg Glu Ile Phe Tyr Glu
 85 90 95

Arg Ser Lys Leu Thr Gly Asn Phe Thr Asp Asp Asn Leu Thr Phe Gln
 100 105 110

Lys Lys Ile Ile Glu Arg Ser Gly Leu Gly Gln Asn Thr Tyr Leu Pro
 115 120 125

Glu Ala Val Leu Arg Val Pro Pro Asn Pro Cys Met Ala Glu Ala Arg
 130 135 140

Lys Glu Ala Glu Met Val Met Phe Gly Ala Ile Asp Glu Leu Leu Glu
 145 150 155 160

Lys Thr Gly Val Lys Pro Lys Asp Ile Gly Ile Leu Val Val Asn Cys
 165 170 175

Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Arg
 180 185 190

Tyr Lys Leu Arg Gly Asn Ile Ile Ser Tyr Asn Leu Gly Gly Met
 195 200 205

<210> 30
 <211> 11
 <212> PRT
 <213> *Simmondsia chinensis*

<400> 30
 Glu Thr Tyr Val Pro Glu Ser Val Thr Lys Lys
 1 5 10

<210> 31
 <211> 10
 <212> PRT
 <213> *Simmondsia chinensis*

<220>
 <221> MOD_RES
 <222> (3)
 <223> Unknown

<220>
 <221> MOD_RES
 <222> (10)
 <223> Unknown

<400> 31
 Val Pro Xaa Glu Pro Ser Ile Ala Ala Xaa
 1 5 10

<210> 32
 <211> 10
 <212> PRT
 <213> *Simmondsia chinensis*

<400> 32
 Glu Thr Tyr Val Pro Glu Glu Val Thr Lys
 1 5 10

<210> 33
 <211> 11
 <212> PRT
 <213> *Simmondsia chinensis*

<400> 33
 Asp Leu Met Ala Val Ala Gly Glu Ala Leu Lys
 1 5 10

<210> 34
 <211> 11
 <212> PRT
 <213> *Simmondsia chinensis*

<400> 34
 Met Thr Asn Val Lys Pro Tyr Ile Pro Asp Phe
 1 5 10

<210> 35
 <211> 11
 <212> PRT
 <213> *Simmondsia chinensis*

<220>
 <221> MOD_RES
 <222> (4)..(5)
 <223> Unknown

<400> 35
 Phe Leu Pro Xaa Xaa Val Ala Ile Thr Gly Glu
 1 5 10

<210> 36
 <211> 17
 <212> PRT
 <213> *Simmondsia chinensis*

<220>
 <221> MOD_RES
 <222> (7)..(8)
 <223> Unknown

<220>
 <221> MOD_RES
 <222> (11)
 <223> Unknown

<400> 36
 Phe Gly Asn Thr Ser Ser Xaa Xaa Leu Tyr Xaa Glu Leu Ala Tyr Ala
 1 5 10 15

Lys

<210> 37
 <211> 17
 <212> PRT
 <213> *Simmondsia chinensis*

<400> 37

Ala Glu Ala Glu Glu Val Met Tyr Gly Ala Ile Asp Glu Val Leu Glu
 1 5 10 15

Lys

<210> 38

<211> 23

<212> PRT

<213> *Acinetobacter* sp.

<220>

<221> MOD_RES

<222> (1)

<223> Unknown

<220>

<221> MOD_RES

<222> (17)

<223> Unknown

<400> 38

Xaa Asp Ile Ala Ile Ile Gly Ser Gly Ser Ala Gly Leu Ala Gln Ala
 1 5 10 15

Xaa Ile Leu Lys Asp Ala Gly
 20

<210> 39

<211> 13

<212> PRT

<213> *Acinetobacter* sp.

<220>

<221> MOD_RES

<222> (7)

<223> Unknown

<400> 39

Gln Gln Phe Thr Val Trp Xaa Asn Ala Ser Glu Pro Ser
 1 5 10

<210> 40

<211> 6

<212> PRT

<213> *Simmondsia chinensis*

<400> 40
 Asn Ile Thr Thr Leu Gly
 1 5

<210> 41
 <211> 6
 <212> PRT
 <213> *Simmondsia chinensis*

<400> 41
 Ser Asn Cys Lys Phe Gly
 1 5

<210> 42
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<220>
 <221> modified_base
 <222> (9)
 <223> a, c, t, g, other or unknown

<220>
 <221> modified_base
 <222> (12)
 <223> a, c, t, g, other or unknown

<220>
 <221> modified_base
 <222> (15)
 <223> a, c, t, g, other or unknown

<400> 42
 aayathacna cnytnngg

17

<210> 43
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<220>
 <221> modified_base
 <222> (15)
 <223> a, c, t, g, other or unknown

<400> 43
 swrttrcayt traancc

17

<210> 44
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Combined DNA/RNA Molecule:
 Synthetic primer

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 44
 caucauac augtcgacaa aatgacgtcc attaacgtaa ag

42

<210> 45
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Combined DNA/RNA Molecule:
 Synthetic primer

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 45
 cuacuacuac uagtcgacgg atcctatttg gaagctttga cattgtttag

50

<210> 46
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<220>
 <221> MOD_RES
 <222> (3)
 <223> Leu or Gly

<400> 46
 Lys Leu Xaa Tyr His Tyr
 1 5

<210> 47
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Combined DNA/RNA Molecule:
 Synthetic primer

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<220>
 <221> modified_base
 <222> (30)
 <223> a, c, t, g, other or unknown

<220>
 <221> modified_base
 <222> (33)
 <223> a, c, t, g, other or unknown

<400> 47
 caucaucauc augaattcaa gcttaarytn bkntaycayt a

41

<210> 48
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 48
 Asn Leu Gly Gly Met Gly Cys
 1 5

<210> 49
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Combined DNA/RNA Molecule:
 Synthetic primer

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<220>
 <221> modified_base
 <222> (30)
 <223> a, c, t, g, other or unknown

<220>
 <221> modified_base
 <222> (33)
 <223> a, c, t, g, other or unknown

<220>
 <221> modified_base
 <222> (36)
 <223> a, c, t, g, other or unknown

<400> 49
 caucaucauc augaattcaa gcttaayytn ggnggnatgg g

41

<210> 50
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Combined DNA/RNA Molecule:
 Synthetic primer

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<220>
 <221> modified_base
 <222> (29)
 <223> a, c, t, g, other or unknown

<220>
 <221> modified_base
 <222> (32)
 <223> a, c, t, g, other or unknown

<220>
 <221> modified_base
 <222> (35)
 <223> a, c, t, g, other or unknown

<400> 50
 cuacuacuac uaggatccgt cgacccatnc cncnarrtt

40

<210> 51
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 51
 Gly Phe Lys Cys Asn Ser
 1 5

<210> 52
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Combined DNA/RNA Molecule:
 Synthetic primer

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<220>
 <221> modified_base
 <222> (39)
 <223> a, c, t, g, other or unknown

<400> 52
 cuacuacuac uaggatccgt cgacswrttr cayttraanc c

41

<210> 53
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Combined DNA/RNA Molecule:
 Synthetic primer

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<220>
<221> modified_base
<222> (27)
<223> a, c, t, g, other or unknown

<400> 53
cuacuacuac uaswrttrca yttraancc